GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 25, 2002, 09:49:41 ; Search time 32.67 Seconds
(without alignments)
1115.158 Million cell updates/sec

Title: US-09-184-826-2
Perfect score: 328
Sequence: 1 MMQDLRLILIIVGAIAIIAL.....TPQKLREYQDIIREVKDANA 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_032802:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	328	19	AAW36984	E. coli ZipA prote
2	227	69.2	328	22	AAG65926	E. coli ZipA prote
3	182	55.5	864	22	ABG21781	Novel human diagno
4	117	35.7	144	22	AAG65925	E. coli ZipA prote
5	21	6.4	328	22	AAG65927	S. typhi ZipA prot
6	11	3.4	328	22	AAG65928	Y. pestis ZipA pro
7	9	2.7	522	20	AAW81571	Mus dunni endogeno
8	9	2.7	622	20	AAW81570	Mus dunni endogeno
9	8	2.4	36	22	AAO03175	Human polypeptide
10	8	2.4	41	22	AAM87430	Human immune/haema
11	8	2.4	42	22	AAO13330	Human polypeptide
12	8	2.4	44	22	AAO13438	Human polypeptide
13	8	2.4	45	22	ABG05119	Novel human diagno
14	8	2.4	45	22	AAO13238	Human polypeptide
15	8	2.4	46	22	AAO02012	Human polypeptide
16	8	2.4	46	22	AAO13301	Human polypeptide
17	8	2.4	46	22	AAO13371	Human polypeptide
18	8	2.4	47	22	AAO11321	Human polypeptide
19	8	2.4	48	22	AAO12235	Human polypeptide
20	8	2.4	48	22	AAO13324	Human polypeptide
21	8	2.4	49	22	AAM82671	Human immune/haema
22	8	2.4	51	22	AAO13292	Human polypeptide
23	8	2.4	52	22	AAO11267	Human polypeptide
24	8	2.4	53	22	AAO02933	Human polypeptide
25	8	2.4	55	22	AAO07312	Human polypeptide
26	8	2.4	55	22	AAO11261	Human polypeptide
27	8	2.4	56	22	AAM83482	Human immune/haema
28	8	2.4	57	22	AAU32261	Novel human secret
29	8	2.4	57	22	AAO02004	Human polypeptide
30	8	2.4	58	22	AAO00928	Human polypeptide
31	8	2.4	58	22	AAO09102	Human polypeptide
32	8	2.4	59	22	AAM82906	Human immune/haema
33	8	2.4	59	22	AAM91350	Human immune/haema
34	8	2.4	59	22	AAO11369	Human polypeptide
35	8	2.4	60	22	AAO08264	Human polypeptide
36	8	2.4	60	22	AAO12892	Human polypeptide
37	8	2.4	61	22	AAU29820	Novel human secret
38	8	2.4	61	22	AAM88413	Human immune/haema
39	8	2.4	62	22	AAU31244	Novel human secret
40	8	2.4	65	22	AAO10147	Human polypeptide
41	8	2.4	70	22	AAU57672	Propionibacterium
42	8	2.4	71	22	AAM84721	Human immune/haema
43	8	2.4	75	22	AAO10281	Human polypeptide
44	8	2.4	77	22	AAM82766	Human immune/haema
45	8	2.4	78	22	AAM87504	Human immune/haema
46	8	2.4	79	22	AAM89885	Human immune/haema
47	8	2.4	86	22	AAG78222	Human DNA mismatch
48	8	2.4	102	22	AAO00087	Human polypeptide
49	8	2.4	104	22	AAO13240	Human polypeptide
50	8	2.4	107	22	AAM82823	Human immune/haema
51	8	2.4	108	22	AAU29906	Novel human secret
52	8	2.4	110	22	AAO10290	Human polypeptide
53	8	2.4	116	22	AAO11339	Human polypeptide
54	8	2.4	133	22	AAO09775	Human polypeptide
55	8	2.4	204	22	AAB93105	Human protein sequ
56	8	2.4	441	21	AAY69524	Xenopus neuroregen
57	8	2.4	620	22	ABB69938	Drosophila melanog
58	8	2.4	635	22	ABG24694	Novel human diagno
59	8	2.4	1476	22	ABB58706	Drosophila melanog
60	8	2.4	2485	21	AAB18172	Plasmodium falcipa
61	7	2.1	17	21	AAB56605	Human prostate can
62	7	2.1	30	22	AAO05096	Human polypeptide
63	7	2.1	32	22	AAO13313	Human polypeptide
64	7	2.1	36	22	AAO08134	Human polypeptide
65	7	2.1	39	22	AAO02750	Human polypeptide
66	7	2.1	41	22	AAO13305	Human polypeptide
67	7	2.1	41	22	AAO13380	Human polypeptide
68	7	2.1	42	22	AAO08190	Human polypeptide
69	7	2.1	43	22	AAO13139	Human polypeptide
70	7	2.1	44	22	ABG05898	Novel human diagno
71	7	2.1	44	22	AAO09036	Human polypeptide
72	7	2.1	44	22	AAO09755	Human polypeptide
73	7	2.1	45	22	AAO07898	Human polypeptide
74	7	2.1	47	22	AAO13250	Human polypeptide
75	7	2.1	48	22	ABB14927	Human nervous syst
76	7	2.1	48	22	AAU31261	Novel human secret
77	7	2.1	49	22	AAM87816	Human immune/haema
78	7	2.1	49	22	AAO10872	Human polypeptide
79	7	2.1	51	22	AAM82946	Human immune/haema
80	7	2.1	51	22	AAO11191	Human polypeptide
81	7	2.1	54	22	AAU31417	Novel human secret
82	7	2.1	59	22	AAO11590	Human polypeptide
83	7	2.1	61	22	AAM82759	Human immune/haema
84	7	2.1	61	22	AAO13159	Human polypeptide

85	7	2.1	63	22	AAU31255	Novel human secret
86	7	2.1	63	22	AAM89589	Human immune/haema
87	7	2.1	64	22	AAU31291	Novel human secret
88	7	2.1	66	22	AAO08161	Human polypeptide
89	7	2.1	67	22	AAM91328	Human immune/haema
90	7	2.1	68	22	ABB10869	Human ovarian and/
91	7	2.1	68	22	AAM95688	Human reproductive
92	7	2.1	68	22	AAM91606	Human immune/haema
93	7	2.1	70	22	AAO05962	Human polypeptide
94	7	2.1	80	22	AAU31245	Novel human secret
95	7	2.1	81	22	ABB70451	Drosophila melanog
96	7	2.1	81	22	AAU31246	Novel human secret
97	7	2.1	81	22	AAM85296	Human immune/haema
98	7	2.1	81	22	AAO11456	Human polypeptide
99	7	2.1	82	22	ABB17455	Human nervous syst
100	7	2.1	82	22	AAO03440	Human polypeptide
101	7	2.1	82	22	AAO09921	Human polypeptide
102	7	2.1	85	22	AAM82715	Human immune/haema
103	7	2.1	86	22	ABB16536	Human nervous syst
104	7	2.1	87	21	AAG02575	Human secreted pro
105	7	2.1	92	22	AAO09773	Human polypeptide
106	7	2.1	96	22	AAO10039	Human polypeptide
107	7	2.1	100	22	AAO12825	Human polypeptide
108	7	2.1	108	22	AAO11505	Human polypeptide
109	7	2.1	112	21	AAY55843	P. ciferrii serine
110	7	2.1	113	22	AAM83410	Human immune/haema
111	7	2.1	118	22	ABG23223	Novel human diagno
112	7	2.1	120	22	AAU29870	Novel human secret
113	7	2.1	128	21	AAG33256	Zea mays protein f
114	7	2.1	131	21	AAG01801	Human secreted pro
115	7	2.1	142	22	AAM24261	Human EST encoded
116	7	2.1	144	21	AAG18062	Arabidopsis thalia
117	7	2.1	148	18	AAW31605	Calcitonin gene re
118	7	2.1	149	21	AAG18061	Arabidopsis thalia
119	7	2.1	157	22	AAM38747	Human polypeptide
120	7	2.1	160	22	AAM40533	Human polypeptide
121	7	2.1	170	21	AAG41297	Arabidopsis thalia
122	7	2.1	170	22	ABB17244	Human nervous syst
123	7	2.1	199	22	AAB68517	Human GTP-binding
124	7	2.1	222	20	AAY37757	Chlamydia trachoma
125	7	2.1	223	22	ABB68114	Drosophila melanog
126	7	2.1	245	21	AAG37622	Arabidopsis thalia
127	7	2.1	245	21	AAG39197	Arabidopsis thalia
128	7	2.1	246	20	AAY19940	B. burgdorferi ant
129	7	2.1	251	21	AAB25671	Human secreted pro
130	7	2.1	252	22	AAB93763	Human protein sequ
131	7	2.1	267	19	AAW81726	M. tuberculosis im
132	7	2.1	267	19	AAW64359	Mycobacterium tube
133	7	2.1	267	20	AAY39156	M. tuberculosis an
134	7	2.1	267	20	AAY39013	M. tuberculosis re
135	7	2.1	274	21	AAG39196	Arabidopsis thalia
136	7	2.1	281	22	AAG81313	Human AFP protein
137	7	2.1	289	22	AAG65930	P. aeruginosa ZipA
138	7	2.1	301	22	AAG90500	C glutamicum prote
139	7	2.1	318	22	AAU64426	Propionibacterium
140	7	2.1	335	21	AAY99350	Human PRO1378 (UNQ
141	7	2.1	335	22	AAU29110	Human PRO polypept
142	7	2.1	335	22	AAB66099	Protein of the inv
143	7	2.1	342	22	AAU55616	Propionibacterium
144	7	2.1	344	22	AAG65929	S. putri ZipA prot
145	7	2.1	356	17	AAW03136	Herpesvirus of tur
146	7	2.1	356	17	AAW03323	Herpesvirus of tur
147	7	2.1	361	22	ABB68291	Drosophila melanog
148	7	2.1	366	22	AAM79122	Human protein SEQ
149	7	2.1	382	22	AAM80106	Human protein SEQ
150	7	2.1	392	22	AAE04176	Human gene 2 encod
151	7	2.1	401	20	AAY17219	Human secreted pro
152	7	2.1	401	22	AAU38989	Human secreted pro
153	7	2.1	401	22	AAB93152	Human protein sequ
154	7	2.1	404	22	AAG82055	S. epidermidis ope
155	7	2.1	414	22	AAE04125	Human gene 2 encod
156	7	2.1	427	19	AAW29661	Homo sapiens CI542
157	7	2.1	467	22	ABG29595	Novel human diagno
158	7	2.1	503	12	AAR14768	Metastasis-specifi
159	7	2.1	571	21	AAB18914	A novel polypeptid
160	7	2.1	571	21	AAY71107	Human Hydrolase pr
161	7	2.1	571	22	AAU12442	Human PRO1887 poly
162	7	2.1	571	22	AAE04101	Human gene 2 encod
163	7	2.1	634	22	ABG01904	Novel human diagno
164	7	2.1	636	22	AAB50659	C. elegans UNC-5 p
165	7	2.1	683	22	AAG92931	C glutamicum prote
166	7	2.1	688	21	AAY57898	Human transmembran
167	7	2.1	696	22	ABB60920	Drosophila melanog
168	7	2.1	717	22	AAB31581	Amino acid sequenc
169	7	2.1	818	22	AAG92737	C glutamicum prote
170	7	2.1	856	21	AAB27656	Human protein PRO3
171	7	2.1	1006	19	AAW70525	Human thymus recep
172	7	2.1	1006	19	AAW72256	Human receptor typ
173	7	2.1	1021	19	AAW70526	Human thymus recep
174	7	2.1	1049	22	ABB71939	Drosophila melanog
175	7	2.1	1123	22	ABB59522	Drosophila melanog
176	7	2.1	1144	22	AAB50658	C. elegans UNC-5 p
177	7	2.1	1191	22	ABG12436	Novel human diagno
178	7	2.1	1233	22	ABB69686	Drosophila melanog
179	7	2.1	2274	22	ABB58657	Drosophila melanog
180	7	2.1	2977	22	ABB69480	Drosophila melanog
181	7	2.1	5533	22	ABB65772	Drosophila melanog
182	7	2.1	5560	22	ABB71160	Drosophila melanog
183	6	1.8	10	16	AAR93331	YES protein tyrosi
184	6	1.8	11	22	AAU08806	Breast cancer cell
185	6	1.8	11	22	AAU25805	Breast cancer-asso
186	6	1.8	12	21	AAB18815	Immunogenic peptid
187	6	1.8	13	22	AAM98136	Human peptide #141
188	6	1.8	14	21	AAY51020	Polio virus B deri
189	6	1.8	20	21	AAB33936	Human secreted pro
190	6	1.8	20	21	AAY53681	Peptide sequence 1
191	6	1.8	20	21	AAY53684	Peptide sequence 1
192	6	1.8	20	21	AAY53685	Peptide 134-153;E1
193	6	1.8	20	22	AAU01826	Gamma gliadin T-ce
194	6	1.8	20	22	AAU01426	Peptide #12 derive
195	6	1.8	23	10	AAP90452	Epitope recognised
196	6	1.8	24	17	AAR87649	Synthetic Bordetel
197	6	1.8	27	22	AAO11471	Human polypeptide
198	6	1.8	30	21	AAB45157	Human secreted pro
199	6	1.8	31	12	AAR11737	Peptide 683 derive
200	6	1.8	31	12	AAR11739	Peptide BBO5 deriv
201	6	1.8	32	22	ABB38903	Peptide #6409 enco
202	6	1.8	32	22	ABB23896	Protein #5895 enco
203	6	1.8	32	22	AAM59554	Human brain expres
204	6	1.8	32	22	AAM72123	Human bone marrow
205	6	1.8	32	22	AAM19447	Peptide #5881 enco
206	6	1.8	32	22	AAM32385	Peptide #6422 enco
207	6	1.8	33	22	ABB40232	Peptide #7738 enco
208	6	1.8	33	22	AAM61011	Human brain expres
209	6	1.8	33	22	AAM73706	Human bone marrow
210	6	1.8	33	22	AAM33892	Peptide #7929 enco
211	6	1.8	34	21	AAB56332	Human secreted pro
212	6	1.8	34	22	ABB40280	Peptide #7786 enco
213	6	1.8	34	22	AAM61073	Human brain expres
214	6	1.8	34	22	AAM73776	Human bone marrow
215	6	1.8	34	22	AAM33963	Peptide #8000 enco
216	6	1.8	38	21	AAB33781	Human secreted pro
217	6	1.8	38	22	AAO08223	Human polypeptide
218	6	1.8	39	21	AAB34645	Gene 13 human secr
219	6	1.8	39	22	AAU22337	Human cardiovascul
220	6	1.8	39	22	AAO07416	Human polypeptide
221	6	1.8	40	18	AAW10968	Polyclonal anti-fe
222	6	1.8	40	22	AAO11155	Human polypeptide
223	6	1.8	41	21	AAB56544	Human prostate can
224	6	1.8	41	22	ABB40647	Peptide #8153 enco
225	6	1.8	41	22	ABB24904	Protein #6903 enco
226	6	1.8	41	22	AAM61507	Human brain expres
227	6	1.8	41	22	AAM74296	Human bone marrow
228	6	1.8	41	22	AAM20261	Peptide #6695 enco
229	6	1.8	41	22	AAM34408	Peptide #8445 enco
230	6	1.8	42	16	AAR65288	Beta amyloid pepti

231	6	1.8	42	22	AAO13326	Human polypeptide
232	6	1.8	43	22	AAO07301	Human polypeptide
233	6	1.8	43	22	AAG62252	Human secreted-pro
234	6	1.8	44	21	AAB29911	Human secreted pro
235	6	1.8	44	21	AAB34112	Human secreted pro
236	6	1.8	44	22	AAO12434	Human polypeptide
237	6	1.8	46	21	AAB34955	Gene 29 human secr
238	6	1.8	46	22	ABB30804	Peptide #3455 enco
239	6	1.8	46	22	ABB35981	Peptide #3487 enco
240	6	1.8	46	22	ABB21391	Protein #3390 enco
241	6	1.8	46	22	AAM56783	Human brain expres
242	6	1.8	46	22	AAM69161	Human bone marrow
243	6	1.8	46	22	AAM16992	Peptide #3426 enco
244	6	1.8	46	22	AAM29484	Peptide #3521 enco
245	6	1.8	46	22	AAM04699	Peptide #3381 enco
246	6	1.8	48	22	AAM87831	Human immune/haema
247	6	1.8	48	22	AAO13208	Human polypeptide
248	6	1.8	48	22	AAO13267	Human polypeptide
249	6	1.8	49	22	AAM89153	Human immune/haema
250	6	1.8	49	22	AAO10780	Human polypeptide
251	6	1.8	50	22	AAG92465	C glutamicum prote
252	6	1.8	50	22	AAG62178	Human gene 23-enco
253	6	1.8	51	22	AAU56825	Propionibacterium
254	6	1.8	51	22	ABB31465	Peptide #4116 enco
255	6	1.8	51	22	ABB36675	Peptide #4181 enco
256	6	1.8	51	22	ABB22011	Protein #4010 enco
257	6	1.8	51	22	AAM54816	Human brain expres
258	6	1.8	51	22	AAM57438	Human brain expres
259	6	1.8	51	22	AAM69835	Human bone marrow
260	6	1.8	51	22	AAM17658	Peptide #4092 enco
261	6	1.8	51	22	AAM30176	Peptide #4213 enco
262	6	1.8	51	22	AAM05318	Peptide #4000 enco
263	6	1.8	52	22	AAU50961	Propionibacterium
264	6	1.8	53	22	AAB64820	Human secreted pro
265	6	1.8	53	22	AAB37886	AGRP-1 protein. S
266	6	1.8	54	22	ABB38795	Peptide #6301 enco
267	6	1.8	54	22	ABB23827	Protein #5826 enco
268	6	1.8	54	22	AAM59434	Human brain expres
269	6	1.8	54	22	AAM71994	Human bone marrow
270	6	1.8	54	22	AAM19397	Peptide #5831 enco
271	6	1.8	54	22	AAM32267	Peptide #6304 enco
272	6	1.8	55	22	AAU56731	Propionibacterium
273	6	1.8	55	22	AAM82725	Human immune/haema
274	6	1.8	57	21	AAG12378	Zea mays protein f
275	6	1.8	57	22	ABB70588	Drosophila melanog
276	6	1.8	58	20	AAY25753	Human secreted pro
277	6	1.8	58	22	AAU67404	Propionibacterium
278	6	1.8	59	16	AAR73922	B.catarrhalis CD e
279	6	1.8	59	21	AAB33893	Human secreted pro
280	6	1.8	59	22	ABG11231	Novel human diagno
281	6	1.8	60	22	AAU59902	Propionibacterium
282	6	1.8	60	22	ABB03492	Human musculoskele
283	6	1.8	60	22	AAO10971	Human polypeptide
284	6	1.8	62	21	AAB39027	Human secreted pro
285	6	1.8	62	22	ABG19857	Novel human diagno
286	6	1.8	63	22	ABG20392	Novel human diagno
287	6	1.8	63	22	ABG26590	Novel human diagno
288	6	1.8	63	22	AAE05256	Mouse Nope (neighb
289	6	1.8	64	22	AAU58572	Propionibacterium
290	6	1.8	64	22	ABG14055	Novel human diagno
291	6	1.8	65	21	AAG02511	Human secreted pro
292	6	1.8	65	22	AAM87348	Human immune/haema
293	6	1.8	67	21	AAB56331	Human secreted pro
294	6	1.8	67	22	AAU23420	Novel human enzyme
295	6	1.8	67	22	AAU16955	Human novel secret
296	6	1.8	68	22	ABG05266	Novel human diagno
297	6	1.8	68	22	AAU31223	Novel human secret
298	6	1.8	69	19	AAW62767	Streptococcus pneu
299	6	1.8	70	22	AAU61615	Propionibacterium
300	6	1.8	70	22	ABB39362	Peptide #6868 enco
301	6	1.8	70	22	ABB24153	Protein #6152 enco
302	6	1.8	70	22	AAM60040	Human brain expres
303	6	1.8	70	22	AAM72643	Human bone marrow
304	6	1.8	70	22	AAM82316	Human immune/haema
305	6	1.8	70	22	AAM19662	Peptide #6096 enco
306	6	1.8	70	22	AAM32877	Peptide #6914 enco
307	6	1.8	71	22	AAU44863	Propionibacterium
308	6	1.8	72	22	AAU63849	Propionibacterium
309	6	1.8	73	19	AAW60154	M. vaccae antigen
310	6	1.8	73	20	AAY14901	M. vaccae antigen
311	6	1.8	73	22	ABG25287	Novel human diagno
312	6	1.8	73	22	ABB43653	Peptide #11159 enc
313	6	1.8	73	22	ABB26604	Protein #8603 enco
314	6	1.8	73	22	AAM64601	Human brain expres
315	6	1.8	73	22	AAM77392	Human bone marrow
316	6	1.8	73	22	AAM21320	Peptide #7754 enco
317	6	1.8	73	22	AAM37547	Peptide #11584 enc
318	6	1.8	74	21	AAG01095	Human secreted pro
319	6	1.8	74	21	AAG01404	Human secreted pro
320	6	1.8	74	22	AAM89738	Human immune/haema
321	6	1.8	76	22	AAM91081	Human immune/haema
322	6	1.8	77	22	AAU50172	Propionibacterium
323	6	1.8	78	19	AAW73149	Bovine amphireguli
324	6	1.8	78	22	AAM91295	Human immune/haema
325	6	1.8	78	22	AAO11230	Human polypeptide
326	6	1.8	79	20	AAY22526	Yeast PABP#3 prote
327	6	1.8	79	22	AAU47704	Propionibacterium
328	6	1.8	79	22	ABB11661	Human secreted pro
329	6	1.8	80	21	AAG58222	Arabidopsis thalia
330	6	1.8	80	22	AAU52512	Propionibacterium
331	6	1.8	80	22	AAO07549	Human polypeptide
332	6	1.8	81	22	AAO07707	Human polypeptide
333	6	1.8	82	10	AAP95451	Protein sequence e
334	6	1.8	82	19	AAW73153	Human amphiregulin
335	6	1.8	82	19	AAW73154	Human amphiregulin
336	6	1.8	83	17	AAR95150	Collagen like prot
337	6	1.8	83	22	AAB72775	Repetitive protein
338	6	1.8	83	22	AAB64045	CLP/CB-F-L2 functi
339	6	1.8	84	10	AAP90449	Sequence of mature
340	6	1.8	85	21	AAG55714	Arabidopsis thalia
341	6	1.8	85	21	AAG55923	Arabidopsis thalia
342	6	1.8	85	21	AAG60730	Arabidopsis thalia
343	6	1.8	86	21	AAG01818	Human secreted pro
344	6	1.8	88	22	ABG23994	Novel human diagno
345	6	1.8	88	22	AAU20670	Human novel foetal
346	6	1.8	88	22	AAM90638	Human immune/haema
347	6	1.8	88	22	AAO10865	Human polypeptide
348	6	1.8	89	21	AAB40881	Human ORFX ORF645
349	6	1.8	90	22	AAU43517	Propionibacterium
350	6	1.8	90	22	AAU63100	Propionibacterium
351	6	1.8	91	18	AAW37304	Amphiregulin AR97-
352	6	1.8	91	21	AAG34427	Arabidopsis thalia
353	6	1.8	96	22	ABG25845	Novel human diagno
354	6	1.8	96	22	ABB27873	Human peptide #524
355	6	1.8	96	22	ABB33044	Peptide #550 encod
356	6	1.8	96	22	AAM66229	Human bone marrow
357	6	1.8	96	22	AAM14099	Peptide #533 encod
358	6	1.8	96	22	AAM26506	Peptide #543 encod
359	6	1.8	96	22	AAM01837	Peptide #519 encod
360	6	1.8	98	22	AAU22330	Human cardiovascul
361	6	1.8	100	21	AAG19094	Zea mays protein f
362	6	1.8	100	21	AAG40677	Zea mays protein f
363	6	1.8	100	22	ABG05262	Novel human diagno
364	6	1.8	101	19	AAY20792	Human neurofilamen
365	6	1.8	101	22	AAM88555	Human immune/haema
366	6	1.8	102	21	AAG37517	Arabidopsis thalia
367	6	1.8	103	21	AAG55713	Arabidopsis thalia
368	6	1.8	104	21	AAB11664	A. vitis hypersens
369	6	1.8	104	21	AAG28787	Arabidopsis thalia
370	6	1.8	104	22	AAM93150	Human digestive sy
371	6	1.8	104	22	AAO09976	Human polypeptide
372	6	1.8	105	21	AAG09341	Arabidopsis thalia
373	6	1.8	105	22	ABG01436	Novel human diagno
374	6	1.8	105	22	ABB12235	Human secreted pro
375	6	1.8	106	21	AAG38617	Arabidopsis thalia
376	6	1.8	106	22	ABG15277	Novel human diagno

377	6	1.8	106	22	ABG18692	Novel human diagno
378	6	1.8	106	22	AAO01772	Human polypeptide
379	6	1.8	107	10	AAP95449	Sequence encoded b
380	6	1.8	107	22	ABB17511	Human nervous syst
381	6	1.8	111	22	AAO09691	Human polypeptide
382	6	1.8	111	22	AAM23490	Human EST encoded
383	6	1.8	112	21	AAG02448	Human secreted pro
384	6	1.8	115	21	AAG19075	Zea mays protein f
385	6	1.8	115	22	AAG73696	Human colon cancer
386	6	1.8	116	22	AAU49869	Propionibacterium
387	6	1.8	116	22	AAO10137	Human polypeptide
388	6	1.8	116	22	AAG91102	C glutamicum prote
389	6	1.8	116	22	AAG91996	C glutamicum prote
390	6	1.8	117	22	ABB70510	Drosophila melanog
391	6	1.8	117	22	AAM24083	A pernix EST encod
392	6	1.8	118	21	AAG58221	Arabidopsis thalia
393	6	1.8	119	22	ABG06840	Novel human diagno
394	6	1.8	119	22	AAM85550	Human immune/haema
395	6	1.8	120	20	AAW93160	Human Lefty-2 prot
396	6	1.8	120	21	AAG12157	Arabidopsis thalia
397	6	1.8	122	18	AAW14565	Streptococcus pneu
398	6	1.8	122	21	AAY94757	Yeast YJL011Cp que
399	6	1.8	124	18	AAW14582	Streptococcus pneu
400	6	1.8	124	21	AAB34366	Gene 10 human secr
401	6	1.8	124	21	AAY76113	Murine cell wall p
402	6	1.8	124	22	AAO04325	Human polypeptide
403	6	1.8	124	22	AAB56052	Skin cell protein,
404	6	1.8	128	18	AAW14577	Streptococcus pneu
405	6	1.8	128	21	AAB51684	Human secreted pro
406	6	1.8	128	21	AAB39172	Human secreted pro
407	6	1.8	129	22	AAO06247	Human polypeptide
408	6	1.8	129	22	AAB92877	Human protein sequ
409	6	1.8	130	20	AAY15226	Human receptor pro
410	6	1.8	130	22	AAU44186	Propionibacterium
411	6	1.8	131	18	AAW14583	Streptococcus pneu
412	6	1.8	131	20	AAY59718	Secreted protein 7
413	6	1.8	131	21	AAG12156	Arabidopsis thalia
414	6	1.8	131	22	AAB64639	Human secreted pro
415	6	1.8	132	21	AAG00109	Human secreted pro
416	6	1.8	133	22	ABG19681	Novel human diagno
417	6	1.8	133	22	AAM87567	Human immune/haema
418	6	1.8	133	22	AAO02565	Human polypeptide
419	6	1.8	134	18	AAW14585	Streptococcus pneu
420	6	1.8	134	21	AAY75490	Neisseria meningit
421	6	1.8	134	22	AAU68574	Human novel cytoki
422	6	1.8	136	21	AAB56611	Human prostate can
423	6	1.8	136	22	ABG28035	Novel human diagno
424	6	1.8	137	21	AAG19093	Zea mays protein f
425	6	1.8	137	22	AAM25517	Human protein sequ
426	6	1.8	138	21	AAB52184	Human secreted pro
427	6	1.8	138	22	AAM95453	Human reproductive
428	6	1.8	139	20	AAY19643	SEQ ID NO 361 from
429	6	1.8	139	21	AAY75491	Neisseria meningit
430	6	1.8	139	21	AAY75513	Neisseria meningit
431	6	1.8	139	21	AAY75514	Neisseria meningit
432	6	1.8	139	22	AAM96463	Human reproductive
433	6	1.8	139	22	AAM40250	Human polypeptide
434	6	1.8	139	22	AAB36627	Human FLEXHT-49 pr
435	6	1.8	140	22	ABG15342	Novel human diagno
436	6	1.8	140	22	AAO01291	Human polypeptide
437	6	1.8	141	21	AAG17012	Arabidopsis thalia
438	6	1.8	141	21	AAG30425	Arabidopsis thalia
439	6	1.8	141	21	AAG37516	Arabidopsis thalia
440	6	1.8	141	22	AAO10166	Human polypeptide
441	6	1.8	144	21	AAG09421	Arabidopsis thalia
442	6	1.8	144	21	AAG11806	Arabidopsis thalia
443	6	1.8	144	21	AAG24084	Arabidopsis thalia
444	6	1.8	144	21	AAG53630	Arabidopsis thalia
445	6	1.8	144	22	ABB10993	Human Ser/Thr kina
446	6	1.8	145	20	AAY37698	Chlamydia trachoma
447	6	1.8	145	22	AAU63250	Propionibacterium
448	6	1.8	146	18	AAW31604	Calcitonin gene re
449	6	1.8	146	19	AAW73159	Human amphiregulin
450	6	1.8	148	18	AAW31606	Calcitonin gene re
451	6	1.8	148	19	AAW46487	Human calcitonin g
452	6	1.8	148	19	AAW50004	Human CGRP-RCF. H
453	6	1.8	148	22	AAU60882	Propionibacterium
454	6	1.8	148	22	ABG07704	Novel human diagno
455	6	1.8	148	22	AAU32258	Novel human secret
456	6	1.8	149	20	AAY07982	Human secreted pro
457	6	1.8	149	22	ABG17169	Novel human diagno
458	6	1.8	150	22	ABB68625	Drosophila melanog
459	6	1.8	151	22	ABG29326	Novel human diagno
460	6	1.8	151	22	AAU01415	Latex allergen Hev
461	6	1.8	152	19	AAW73158	Human amphiregulin
462	6	1.8	152	22	AAU47645	Propionibacterium
463	6	1.8	154	19	AAW98259	H. pylori GHPO 895
464	6	1.8	154	21	AAG19092	Zea mays protein f
465	6	1.8	155	15	AAR45451	Adenovirus E1A-F p
466	6	1.8	155	21	AAG37515	Arabidopsis thalia
467	6	1.8	155	22	AAU49591	Propionibacterium
468	6	1.8	155	22	AAU56468	Propionibacterium
469	6	1.8	155	22	AAM41768	Human polypeptide
470	6	1.8	155	22	AAB68931	Neisseria meningit
471	6	1.8	156	22	AAM42036	Human polypeptide
472	6	1.8	157	22	AAU62368	Propionibacterium
473	6	1.8	158	19	AAW73156	Soluble Human amph
474	6	1.8	158	22	AAU39656	Propionibacterium
475	6	1.8	158	22	AAU44918	Propionibacterium
476	6	1.8	158	22	ABB39858	Peptide #7364 enco
477	6	1.8	158	22	ABB24450	Protein #6449 enco
478	6	1.8	158	22	AAM60590	Human brain expres
479	6	1.8	158	22	AAM73258	Human bone marrow
480	6	1.8	158	22	AAM19901	Peptide #6335 enco
481	6	1.8	158	22	AAM33459	Peptide #7496 enco
482	6	1.8	158	22	AAG91583	C glutamicum prote
483	6	1.8	158	22	AAB79007	C. glutamicum SRT
484	6	1.8	159	8	AAP70494	Sequence of human
485	6	1.8	159	21	AAB11368	E. coli KDTB prote
486	6	1.8	159	21	AAY79301	E. coli phosphopan
487	6	1.8	159	22	ABB66311	Drosophila melanog
488	6	1.8	161	22	AAU37770	Streptococcus pneu
489	6	1.8	161	22	AAU38022	Streptococcus pneu
490	6	1.8	161	22	AAU42760	Propionibacterium
491	6	1.8	161	22	AAU56873	Propionibacterium
492	6	1.8	161	22	ABG23981	Novel human diagno
493	6	1.8	161	22	AAM01086	CFE 89 protein seq
494	6	1.8	161	22	AAU19602	Human diagnostic a
495	6	1.8	163	19	AAY85871	S. pneumoniae deri
496	6	1.8	163	21	AAG12155	Arabidopsis thalia
497	6	1.8	164	21	AAB21038	Human nucleic acid
498	6	1.8	164	22	AAU53362	Propionibacterium
499	6	1.8	164	22	AAM39982	Human polypeptide
500	6	1.8	164	22	AAB93367	Human protein sequ
501	6	1.8	165	22	AAU36392	Pseudomonas aerugi
502	6	1.8	166	21	AAG30424	Arabidopsis thalia
503	6	1.8	166	22	AAB94660	Human protein sequ
504	6	1.8	167	22	ABG22443	Novel human diagno
505	6	1.8	168	22	AAU16951	Human novel secret
506	6	1.8	169	22	ABG04715	Novel human diagno
507	6	1.8	172	21	AAG55367	Arabidopsis thalia
508	6	1.8	172	22	AAG74761	Human colon cancer
509	6	1.8	174	21	AAG11477	Arabidopsis thalia
510	6	1.8	175	19	AAW77365	zsig10 polypeptide
511	6	1.8	175	19	AAW37844	Human XAG growth f
512	6	1.8	175	19	AAW37872	Human protein comp
513	6	1.8	175	20	AAY59675	Secreted protein 1
514	6	1.8	175	21	AAB24070	Human PRO1030 prot
515	6	1.8	175	21	AAG30423	Arabidopsis thalia
516	6	1.8	175	22	AAU54995	Propionibacterium
517	6	1.8	175	22	AAU08804	Breast cancer cell
518	6	1.8	175	22	AAB72203	Human huXAG-1/CCSG
519	6	1.8	176	21	AAG26108	Zea mays protein f
520	6	1.8	178	21	AAG11476	Arabidopsis thalia
521	6	1.8	178	22	ABG18621	Novel human diagno
522	6	1.8	179	22	AAU57428	Propionibacterium

523	6	1.8	180	18	AAW14562	Streptococcus pneu
524	6	1.8	180	19	AAW98570	H. pylori GHPO 9 p
525	6	1.8	180	21	AAY91357	Human secreted pro
526	6	1.8	181	22	AAU33595	Pseudomonas aerugi
527	6	1.8	184	18	AAW14589	Streptococcus pneu
528	6	1.8	184	21	AAB16320	Eucalyptus grandis
529	6	1.8	184	22	AAB20257	White spot syndrom
530	6	1.8	185	14	AAR34717	Bacillus subtilis
531	6	1.8	185	18	AAW14566	Streptococcus pneu
532	6	1.8	186	22	ABG09410	Novel human diagno
533	6	1.8	186	22	AAU17024	Human novel secret
534	6	1.8	187	18	AAW14579	Streptococcus pneu
535	6	1.8	187	21	AAG29045	Arabidopsis thalia
536	6	1.8	187	22	AAU18421	Human endocrine po
537	6	1.8	188	18	AAW14580	Streptococcus pneu
538	6	1.8	189	21	AAG33435	Zea mays protein f
539	6	1.8	191	19	AAW38543	S. pneumoniae cyst
540	6	1.8	191	22	AAU54775	Propionibacterium
541	6	1.8	192	21	AAY91976	Murine interferon
542	6	1.8	192	22	ABG19975	Novel human diagno
543	6	1.8	193	22	AAU04899	Micromonospora eve
544	6	1.8	193	22	AAU15093	Protein encoded by
545	6	1.8	194	20	AAY76590	Human ovarian tumo
546	6	1.8	195	18	AAW14591	Streptococcus pneu
547	6	1.8	195	20	AAY07105	Colon cancer assoc
548	6	1.8	195	21	AAG29044	Arabidopsis thalia
549	6	1.8	196	18	AAW14564	Streptococcus pneu
550	6	1.8	197	21	AAG55366	Arabidopsis thalia
551	6	1.8	197	22	ABG28941	Novel human diagno
552	6	1.8	197	22	AAG93076	C glutamicum prote
553	6	1.8	198	18	AAW14581	Streptococcus pneu
554	6	1.8	198	22	AAU28289	Novel human secret
555	6	1.8	199	14	AAR43885	Consensus sequence
556	6	1.8	199	22	ABG05326	Novel human diagno
557	6	1.8	199	22	ABG17356	Novel human diagno
558	6	1.8	199	22	AAM00086	Alpha-glucosidase
559	6	1.8	200	14	AAR43879	C-terminal portion
560	6	1.8	200	21	AAG55365	Arabidopsis thalia
561	6	1.8	200	22	ABG14506	Novel human diagno
562	6	1.8	202	22	AAG75621	Human colon cancer
563	6	1.8	203	21	AAG09340	Arabidopsis thalia
564	6	1.8	204	18	AAW14571	Streptococcus pneu
565	6	1.8	204	18	AAW14578	Streptococcus pneu
566	6	1.8	204	21	AAG38616	Arabidopsis thalia
567	6	1.8	204	22	AAG84978	Shrimp white spot
568	6	1.8	204	22	AAB20261	White spot syndrom
569	6	1.8	205	21	AAB41610	Human ORFX ORF1374
570	6	1.8	205	21	AAG23624	Arabidopsis thalia
571	6	1.8	205	22	AAG91597	C glutamicum prote
572	6	1.8	206	20	AAY73837	Human prostate tum
573	6	1.8	206	22	ABG05794	Novel human diagno
574	6	1.8	206	22	AAB95820	Human protein sequ
575	6	1.8	207	22	ABG09882	Novel human diagno
576	6	1.8	208	21	AAY95314	Corn phosphatidylg
577	6	1.8	208	21	AAY68968	Cps2S protein whic
578	6	1.8	208	22	AAB95022	Human protein sequ
579	6	1.8	209	22	AAU67923	Propionibacterium
580	6	1.8	211	22	AAU52836	Propionibacterium
581	6	1.8	211	22	AAE12080	Dendritic cell (DC
582	6	1.8	212	21	AAG57996	Arabidopsis thalia
583	6	1.8	212	21	AAG61575	Arabidopsis thalia
584	6	1.8	212	22	ABG03224	Novel human diagno
585	6	1.8	212	22	ABG05311	Novel human diagno
586	6	1.8	212	22	ABG05798	Novel human diagno
587	6	1.8	213	22	ABG02504	Novel human diagno
588	6	1.8	213	22	AAB84215	Amino acid sequenc
589	6	1.8	214	22	AAB86467	Crypthecodinium sp
590	6	1.8	214	22	AAB97225	Murine C-type lect
591	6	1.8	217	21	AAG41828	Arabidopsis thalia
592	6	1.8	218	22	AAU58170	Propionibacterium
593	6	1.8	218	22	AAE12079	Dendritic cell (DC
594	6	1.8	219	21	AAG17011	Arabidopsis thalia
595	6	1.8	219	21	AAG41827	Arabidopsis thalia
596	6	1.8	219	22	AAG92035	C glutamicum prote
597	6	1.8	220	21	AAB13569	Streptomyces globi
598	6	1.8	220	21	AAB32549	Eucalyptus grandis
599	6	1.8	221	21	AAG17187	Arabidopsis thalia
600	6	1.8	221	21	AAG52743	Arabidopsis thalia
601	6	1.8	222	21	AAB32874	Pinus radiata tran
602	6	1.8	224	18	AAW36796	Novel human protei
603	6	1.8	226	19	AAW73157	Human amphiregulin
604	6	1.8	227	22	AAU25579	Human G Protein-Co
605	6	1.8	228	21	AAB56645	Human prostate can
606	6	1.8	228	21	AAG22407	Arabidopsis thalia
607	6	1.8	228	22	AAU43682	Propionibacterium
608	6	1.8	230	22	AAU41712	Propionibacterium
609	6	1.8	231	21	AAG57995	Arabidopsis thalia
610	6	1.8	231	21	AAG61574	Arabidopsis thalia
611	6	1.8	232	22	ABG12639	Novel human diagno
612	6	1.8	233	18	AAW14572	Streptococcus pneu
613	6	1.8	233	18	AAW14590	Streptococcus pneu
614	6	1.8	234	21	AAG30349	Arabidopsis thalia
615	6	1.8	236	21	AAB41465	Human ORFX ORF1229
616	6	1.8	237	21	AAG23623	Arabidopsis thalia
617	6	1.8	237	22	AAU14095	Epstein-Barr virus
618	6	1.8	240	21	AAG17333	Arabidopsis thalia
619	6	1.8	240	21	AAG30348	Arabidopsis thalia
620	6	1.8	240	22	AAM90252	Human immune/haema
621	6	1.8	240	22	AAB66648	Mouse tissue facto
622	6	1.8	241	21	AAG36591	Arabidopsis thalia
623	6	1.8	241	22	ABB58090	Drosophila melanog
624	6	1.8	241	22	ABG05800	Novel human diagno
625	6	1.8	241	22	ABG09099	Novel human diagno
626	6	1.8	245	12	AAR11712	Human Stem Cell Fa
627	6	1.8	245	13	AAR20646	Human "Delta 28" m
628	6	1.8	245	16	AAR83979	Human stem cell fa
629	6	1.8	245	22	AAU05267	Human SCF protein
630	6	1.8	245	22	AAB98368	Human SCF protein
631	6	1.8	245	22	AAU02461	Human SCF protein
632	6	1.8	245	22	AAU02767	Human SCF protein
633	6	1.8	245	22	AAB73568	Human SCF protein
634	6	1.8	245	22	AAB96953	Human stem cell fa
635	6	1.8	246	20	AAY34805	Chlamydia pneumoni
636	6	1.8	246	21	AAY53285	Human SCF protein
637	6	1.8	247	19	AAW73160	Bovine amphireguli
638	6	1.8	248	21	AAG54570	Zea mays protein f
639	6	1.8	248	22	AAG67745	Amino acid sequenc
640	6	1.8	250	14	AAR38794	Monoglyceride lipa
641	6	1.8	250	22	ABB61109	Drosophila melanog
642	6	1.8	251	21	AAB43216	Human ORFX ORF2980
643	6	1.8	251	21	AAB16274	Eucalyptus grandis
644	6	1.8	251	22	ABG00658	Novel human diagno
645	6	1.8	251	22	ABG08208	Novel human diagno
646	6	1.8	252	10	AAP95447	Amphiregulin precu
647	6	1.8	253	22	AAB48839	Petunia hybrida ZP
648	6	1.8	254	22	ABG26078	Novel human diagno
649	6	1.8	257	21	AAG22406	Arabidopsis thalia
650	6	1.8	257	21	AAG54569	Zea mays protein f
651	6	1.8	258	12	AAR15227	HincII modificatio
652	6	1.8	258	19	AAW55107	Streptococcus pneu
653	6	1.8	258	21	AAB34197	Gene 35 human secr
654	6	1.8	259	21	AAG17186	Arabidopsis thalia
655	6	1.8	259	21	AAG52742	Arabidopsis thalia
656	6	1.8	260	11	AAR08332	Pseudomonas creati
657	6	1.8	260	17	AAW03520	BalI restriction e
658	6	1.8	260	21	AAG40773	Zea mays protein f
659	6	1.8	260	22	ABB57988	Drosophila melanog
660	6	1.8	263	21	AAG11475	Arabidopsis thalia
661	6	1.8	263	22	ABB64191	Drosophila melanog
662	6	1.8	263	22	ABG25283	Novel human diagno
663	6	1.8	264	22	AAU55613	Propionibacterium
664	6	1.8	265	20	AAY29128	Amino acid sequenc
665	6	1.8	266	22	ABG00609	Novel human diagno
666	6	1.8	266	22	ABG03074	Novel human diagno
667	6	1.8	266	22	ABG06836	Novel human diagno
668	6	1.8	266	22	AAU05263	Stem cell factor (

669	6	1.8	266	22	AAG82440	S. epidermidis ope
670	6	1.8	266	22	AAB98365	Consensus SCF prot
671	6	1.8	266	22	AAU02490	SCF (stem cell fac
672	6	1.8	266	22	AAU02776	SCF (stem cell fac
673	6	1.8	266	22	AAB96950	Stem cell factor S
674	6	1.8	267	22	AAU14624	Novel bone marrow
675	6	1.8	269	22	AAB68501	Human GTP-binding
676	6	1.8	270	21	AAG44643	Zea mays protein f
677	6	1.8	272	21	AAG40772	Zea mays protein f
678	6	1.8	273	12	AAR11711	Human Stem Cell Fa
679	6	1.8	273	13	AAR20647	Human mast cell gr
680	6	1.8	273	14	AAR32166	hKL fragment A. S
681	6	1.8	273	16	AAR83978	Human stem cell fa
682	6	1.8	273	18	AAW27607	Human recombinant
683	6	1.8	273	21	AAY53284	Human SCF protein
684	6	1.8	273	22	AAU05256	Human stem cell fa
685	6	1.8	273	22	AAU05266	Human SCF protein
686	6	1.8	273	22	AAB98356	Human stem cell fa
687	6	1.8	273	22	AAB98357	Human SCF protein
688	6	1.8	273	22	AAB98367	Human SCF protein
689	6	1.8	273	22	AAU02458	Human SCF (stem ce
690	6	1.8	273	22	AAU02460	Human SCF protein
691	6	1.8	273	22	AAU02765	Human SCF (stem ce
692	6	1.8	273	22	AAU02766	Human SCF protein
693	6	1.8	273	22	AAB73566	Human SCF (stem ce
694	6	1.8	273	22	AAB73567	Human SCF protein
695	6	1.8	273	22	AAB96941	Human stem cell fa
696	6	1.8	273	22	AAB96942	Human stem cell fa
697	6	1.8	273	22	AAB96952	Human stem cell fa
698	6	1.8	274	22	ABG00718	Novel human diagno
699	6	1.8	274	22	AAB70071	Human secreted pro
700	6	1.8	275	20	AAW87603	Prepromagainin seq
701	6	1.8	276	20	AAY37171	Amino acid sequenc
702	6	1.8	276	22	ABB59768	Drosophila melanog
703	6	1.8	278	22	AAB65782	Cysteine protease
704	6	1.8	280	19	AAW54379	Cell division cycl
705	6	1.8	281	20	AAW97119	S-adenosyl-L-methy
706	6	1.8	281	21	AAY94924	Human secreted pro
707	6	1.8	282	20	AAW67850	Human secreted pro
708	6	1.8	282	21	AAG41826	Arabidopsis thalia
709	6	1.8	283	22	AAE12979	Pork tapeworm matu
710	6	1.8	284	20	AAY37002	Chlamydia trachoma
711	6	1.8	284	22	AAU28101	Novel human secret
712	6	1.8	284	22	AAM25837	Human protein sequ
713	6	1.8	284	22	AAG93250	Human protein HP02
714	6	1.8	286	21	AAY53041	Human secreted pro
715	6	1.8	286	22	AAU59263	Propionibacterium
716	6	1.8	286	22	AAM80096	Human protein SEQ
717	6	1.8	287	21	AAG44642	Zea mays protein f
718	6	1.8	287	21	AAG53597	Arabidopsis thalia
719	6	1.8	287	22	AAG90436	C glutamicum prote
720	6	1.8	287	22	AAG82613	S. epidermidis ope
721	6	1.8	288	21	AAY95934	Porcine adenovirus
722	6	1.8	288	22	ABB59523	Drosophila melanog
723	6	1.8	288	22	ABB53040	Escherichia coli p
724	6	1.8	288	22	AAB73577	Consensus SCF (ste
725	6	1.8	290	13	AAR28774	MD06 Marek's Disea
726	6	1.8	290	22	AAE12977	Pork tapeworm matu
727	6	1.8	290	22	AAE12978	Pork tapeworm matu
728	6	1.8	292	22	ABG05275	Novel human diagno
729	6	1.8	294	22	ABB62954	Drosophila melanog
730	6	1.8	294	22	ABG17361	Novel human diagno
731	6	1.8	294	22	AAB35940	TGF-beta 4 amino a
732	6	1.8	295	21	AAG28761	Arabidopsis thalia
733	6	1.8	295	21	AAG52964	Arabidopsis thalia
734	6	1.8	296	22	AAG92212	C glutamicum prote
735	6	1.8	298	21	AAG51730	Arabidopsis thalia
736	6	1.8	299	19	AAW61008	Streptococcus pneu
737	6	1.8	299	20	AAY49158	Corn cyclin-depend
738	6	1.8	300	22	ABB58826	Drosophila melanog
739	6	1.8	301	22	AAU40700	Propionibacterium
740	6	1.8	302	22	ABG04249	Novel human diagno
741	6	1.8	303	22	ABB58168	Drosophila melanog
742	6	1.8	303	22	ABG14308	Novel human diagno
743	6	1.8	305	21	AAG05380	Arabidopsis thalia
744	6	1.8	305	21	AAG30828	Arabidopsis thalia
745	6	1.8	305	21	AAG48337	Arabidopsis thalia
746	6	1.8	305	22	AAB62463	Fruit fly Chk1 kin
747	6	1.8	305	22	AAB94143	Human protein sequ
748	6	1.8	307	20	AAY59886	Human normal uteru
749	6	1.8	307	21	AAB19420	A prenyltransferas
750	6	1.8	307	22	AAG81714	S. epidermidis ope
751	6	1.8	309	21	AAG54568	Zea mays protein f
752	6	1.8	309	21	AAY90811	Escherichia coli r
753	6	1.8	309	22	AAU36124	Klebsiella pneumon
754	6	1.8	309	22	ABG03277	Novel human diagno
755	6	1.8	309	22	ABG15065	Novel human diagno
756	6	1.8	309	22	ABG23286	Novel human diagno
757	6	1.8	310	21	AAG06884	Arabidopsis thalia
758	6	1.8	310	21	AAG45676	Arabidopsis thalia
759	6	1.8	310	22	ABG05624	Novel human diagno
760	6	1.8	311	22	ABG05272	Novel human diagno
761	6	1.8	312	21	AAG51729	Arabidopsis thalia
762	6	1.8	313	7	AAP60071	Sequence of the Tr
763	6	1.8	313	22	ABG30282	Novel human diagno
764	6	1.8	314	15	AAR54664	I kappa B like pro
765	6	1.8	314	20	AAY36797	Protein involved i
766	6	1.8	314	21	AAB33224	Eucalyptus grandis
767	6	1.8	314	22	AAU64535	Propionibacterium
768	6	1.8	315	21	AAG13408	Arabidopsis thalia
769	6	1.8	315	22	AAG71656	Human olfactory re
770	6	1.8	316	21	AAG17332	Arabidopsis thalia
771	6	1.8	316	21	AAG27974	Arabidopsis thalia
772	6	1.8	316	22	ABB66952	Drosophila melanog
773	6	1.8	316	22	ABG22433	Novel human diagno
774	6	1.8	316	22	AAM42210	Human polypeptide
775	6	1.8	317	21	AAG36590	Arabidopsis thalia
776	6	1.8	317	21	AAG51728	Arabidopsis thalia
777	6	1.8	317	22	ABG24218	Novel human diagno
778	6	1.8	318	21	AAG48300	Arabidopsis thalia
779	6	1.8	320	21	AAG13407	Arabidopsis thalia
780	6	1.8	321	21	AAB18723	A Neisseria mening
781	6	1.8	321	21	AAY75551	Neisseria meningit
782	6	1.8	321	21	AAY75552	Neisseria meningit
783	6	1.8	322	22	ABB66009	Drosophila melanog
784	6	1.8	323	21	AAY75550	Neisseria gonorrhe
785	6	1.8	323	22	AAU56092	Propionibacterium
786	6	1.8	323	22	AAU32466	Novel human secret
787	6	1.8	324	21	AAB29859	Human secreted pro
788	6	1.8	324	21	AAG17331	Arabidopsis thalia
789	6	1.8	324	22	ABG15077	Novel human diagno
790	6	1.8	325	21	AAB19095	Protein encoded by
791	6	1.8	325	21	AAB35795	Protein involved i
792	6	1.8	325	21	AAG30227	Arabidopsis thalia
793	6	1.8	325	21	AAG36589	Arabidopsis thalia
794	6	1.8	326	19	AAW36985	Haemophilus influe
795	6	1.8	326	22	ABG00257	Novel human diagno
796	6	1.8	326	22	ABB30141	Peptide #2792 enco
797	6	1.8	326	22	ABB35311	Peptide #2817 enco
798	6	1.8	326	22	ABB20753	Protein #2752 enco
799	6	1.8	326	22	AAM56142	Human brain expres
800	6	1.8	326	22	AAM68515	Human bone marrow
801	6	1.8	326	22	AAM16319	Peptide #2753 enco
802	6	1.8	326	22	AAM28814	Peptide #2851 enco
803	6	1.8	326	22	AAM04057	Peptide #2739 enco
804	6	1.8	326	22	AAG75109	Human colon cancer
805	6	1.8	327	6	AAP50046	Hybrid trpE-SS14 p
806	6	1.8	327	22	AAU35605	Haemophilus influe
807	6	1.8	327	22	AAB99096	Rat GnRH receptor
808	6	1.8	327	22	AAB99097	Rat GnRH receptor
809	6	1.8	327	22	AAB99098	Rat GnRH receptor
810	6	1.8	327	22	AAB99099	Rat GnRH receptor
811	6	1.8	327	22	AAB99100	Rat GnRH receptor
812	6	1.8	327	22	AAG62501	Rat GnRH receptor
813	6	1.8	327	22	AAG62502	Rat GnRH receptor
814	6	1.8	327	22	AAG62503	Rat GnRH receptor

815	6	1.8	327	22	AAG62504	Rat GnRH receptor
816	6	1.8	328	17	AAR91225	Human placenta G-p
817	6	1.8	328	18	AAW09433	Human placenta pur
818	6	1.8	328	21	AAG53596	Arabidopsis thalia
819	6	1.8	328	22	AAG65932	H. influenzae ZipA
820	6	1.8	328	22	AAE04393	Human P2-purinergi
821	6	1.8	329	21	AAB35796	Protein involved i
822	6	1.8	329	22	AAG72696	Murine OR-like pol
823	6	1.8	330	21	AAG13406	Arabidopsis thalia
824	6	1.8	330	21	AAY81462	Human ataxin-2 bin
825	6	1.8	331	20	AAY50338	P. fluorescens ICS
826	6	1.8	331	20	AAY14919	Amino acid sequenc
827	6	1.8	331	22	ABG18006	Novel human diagno
828	6	1.8	332	21	AAG30827	Arabidopsis thalia
829	6	1.8	333	22	AAU31751	Novel human secret
830	6	1.8	333	22	AAB79218	Corynebacterium gl
831	6	1.8	334	22	ABB71970	Drosophila melanog
832	6	1.8	334	22	AAU34788	E. coli cellular p
833	6	1.8	335	21	AAG29000	Arabidopsis thalia
834	6	1.8	335	22	AAU30843	Novel human secret
835	6	1.8	337	21	AAY74311	Neisseria gonorrhe
836	6	1.8	337	22	AAU34091	Staphylococcus aur
837	6	1.8	337	22	AAU38207	Salmonella typhi c
838	6	1.8	337	22	ABG10588	Novel human diagno
839	6	1.8	339	22	ABG28871	Novel human diagno
840	6	1.8	339	22	AAU68530	Human novel cytoki
841	6	1.8	340	22	AAU36832	Staphylococcus aur
842	6	1.8	340	22	AAU37545	Staphylococcus aur
843	6	1.8	343	21	AAG27973	Arabidopsis thalia
844	6	1.8	344	22	AAU16460	Human novel secret
845	6	1.8	344	22	AAG72994	Olfactory receptor
846	6	1.8	345	21	AAG14170	Arabidopsis thalia
847	6	1.8	345	21	AAG27431	Arabidopsis thalia
848	6	1.8	345	22	AAG65931	Alpha-actin ZipA p
849	6	1.8	345	22	AAG92830	C glutamicum prote
850	6	1.8	345	22	AAB79347	Corynebacterium gl
851	6	1.8	346	22	ABB70516	Drosophila melanog
852	6	1.8	347	22	ABG14105	Novel human diagno
853	6	1.8	347	22	ABG14206	Novel human diagno
854	6	1.8	347	22	ABG14470	Novel human diagno
855	6	1.8	347	22	AAB61981	S. avermitilis ORF
856	6	1.8	348	22	AAU48382	Propionibacterium
857	6	1.8	349	8	AAP70463	Sequence of gpI en
858	6	1.8	350	20	AAY02170	A Staphylococcus a
859	6	1.8	350	21	AAG57994	Arabidopsis thalia
860	6	1.8	350	21	AAG61573	Arabidopsis thalia
861	6	1.8	350	22	AAU34216	Staphylococcus aur
862	6	1.8	350	22	AAU36879	Staphylococcus aur
863	6	1.8	350	22	AAU65972	Propionibacterium
864	6	1.8	350	22	ABG29329	Novel human diagno
865	6	1.8	351	21	AAY74312	Neisseria meningit
866	6	1.8	352	18	AAW20628	H. pylori cytoplas
867	6	1.8	353	22	ABB68107	Drosophila melanog
868	6	1.8	353	22	ABG10861	Novel human diagno
869	6	1.8	354	20	AAY07104	Colon cancer assoc
870	6	1.8	354	21	AAG09441	Arabidopsis thalia
871	6	1.8	354	21	AAG45209	Arabidopsis thalia
872	6	1.8	355	21	AAY75398	Neisseria meningit
873	6	1.8	355	21	AAY75399	Neisseria meningit
874	6	1.8	356	21	AAG30226	Arabidopsis thalia
875	6	1.8	356	21	AAG34496	Arabidopsis thalia
876	6	1.8	356	22	AAU65391	Propionibacterium
877	6	1.8	356	22	AAU03120	Streptococcus pyog
878	6	1.8	357	15	ABB04127	Fusarium oxysporum
879	6	1.8	357	21	AAY75397	Neisseria gonorrhe
880	6	1.8	357	22	ABG00023	Novel human diagno
881	6	1.8	359	22	ABG05264	Novel human diagno
882	6	1.8	359	22	ABG15053	Novel human diagno
883	6	1.8	359	22	ABG19795	Novel human diagno
884	6	1.8	359	22	ABG23276	Novel human diagno
885	6	1.8	360	21	AAB32575	Eucalyptus grandis
886	6	1.8	360	22	ABG23283	Novel human diagno
887	6	1.8	361	22	AAU33906	Staphylococcus aur
888	6	1.8	361	22	ABG05318	Novel human diagno
889	6	1.8	362	20	AAY35611	Chlamydia pneumoni
890	6	1.8	362	21	AAG09440	Arabidopsis thalia
891	6	1.8	362	21	AAG45208	Arabidopsis thalia
892	6	1.8	362	22	AAG93137	C glutamicum prote
893	6	1.8	363	22	ABB62107	Drosophila melanog
894	6	1.8	363	22	AAB96616	Putative P. abyssi
895	6	1.8	365	20	AAY00205	Enterococcus faeca
896	6	1.8	365	22	ABG04631	Novel human diagno
897	6	1.8	365	22	AAG73503	Human gene 30-enco
898	6	1.8	366	20	AAY17871	Human bone morphog
899	6	1.8	366	21	AAG30826	Arabidopsis thalia
900	6	1.8	366	21	AAG53595	Arabidopsis thalia
901	6	1.8	366	22	AAB95157	Human protein sequ
902	6	1.8	366	22	AAB19837	Endometrial bleedi
903	6	1.8	367	22	ABG05310	Novel human diagno
904	6	1.8	367	22	ABG05795	Novel human diagno
905	6	1.8	367	22	AAU00875	Human cancer relat
906	6	1.8	369	21	AAG14169	Arabidopsis thalia
907	6	1.8	369	21	AAG27430	Arabidopsis thalia
908	6	1.8	370	15	AAR48697	G-protein coupled
909	6	1.8	370	17	AAW02669	G-protein coupled
910	6	1.8	370	21	AAY92013	Human transforming
911	6	1.8	371	21	AAG28999	Arabidopsis thalia
912	6	1.8	372	20	AAY07102	Colon cancer assoc
913	6	1.8	372	21	AAG09439	Arabidopsis thalia
914	6	1.8	372	21	AAG45207	Arabidopsis thalia
915	6	1.8	372	22	AAG92376	C glutamicum prote
916	6	1.8	374	12	AAR13987	Lycopene cyclase -
917	6	1.8	374	17	AAW01125	Lycopene cyclase.
918	6	1.8	374	18	AAW32474	Erwinia herbicola
919	6	1.8	375	21	AAG28998	Arabidopsis thalia
920	6	1.8	376	12	AAR15272	Fusarium oxysporum
921	6	1.8	376	13	AAR25527	Fusarium oxysporum
922	6	1.8	376	13	AAR25466	Endoglucanase #2.
923	6	1.8	376	13	AAR25429	Cellulase containe
924	6	1.8	376	13	AAR27969	Endoglucanase enzy
925	6	1.8	376	14	AAR37151	Dye transfer inhib
926	6	1.8	376	14	AAR42064	Endoglucanase enzy
927	6	1.8	376	16	AAY67389	F. oxysporum endog
928	6	1.8	376	19	AAW46617	Fusarium oxysporum
929	6	1.8	376	22	AAU35314	Enterococcus faeca
930	6	1.8	377	21	AAG27972	Arabidopsis thalia
931	6	1.8	379	10	AAP90508	Sequence of an epi
932	6	1.8	380	10	AAP90509	Sequence of an epi
933	6	1.8	380	10	AAP90510	Sequence of an epi
934	6	1.8	380	10	AAP90511	Sequence of an epi
935	6	1.8	380	10	AAP90512	Sequence of new po
936	6	1.8	381	21	AAG22405	Arabidopsis thalia
937	6	1.8	381	22	AAU35377	Haemophilus influe
938	6	1.8	382	22	ABB64589	Drosophila melanog
939	6	1.8	382	22	ABG03207	Novel human diagno
940	6	1.8	383	19	AAW98461	H. pylori GHPO 718
941	6	1.8	383	21	AAG10770	Arabidopsis thalia
942	6	1.8	386	22	AAU36977	Staphylococcus aur
943	6	1.8	386	22	AAG92871	C glutamicum prote
944	6	1.8	386	22	AAB79610	Corynebacterium gl
945	6	1.8	386	22	AAB79611	Corynebacterium gl
946	6	1.8	386	22	AAB80028	Corynebacterium gl
947	6	1.8	387	22	ABG10857	Novel human diagno
948	6	1.8	388	21	AAG06883	Arabidopsis thalia
949	6	1.8	388	21	AAG45675	Arabidopsis thalia
950	6	1.8	388	22	ABG18035	Novel human diagno
951	6	1.8	390	21	AAG10769	Arabidopsis thalia
952	6	1.8	391	20	AAY50336	P. fluorescens ICS
953	6	1.8	391	22	ABB62644	Drosophila melanog
954	6	1.8	391	22	AAB90766	Human shear stress
955	6	1.8	392	20	AAY00204	Enterococcus faeca
956	6	1.8	392	22	ABG19861	Novel human diagno
957	6	1.8	393	21	AAB57000	Human prostate can
958	6	1.8	395	21	AAG18686	Arabidopsis thalia
959	6	1.8	396	21	AAB21215	cyt/Hpa44/HF fusio
960	6	1.8	396	22	AAU51015	Propionibacterium

961	6	1.8	397	21	AAB43211	Human ORFX ORF2975
962	6	1.8	397	21	AAG06882	Arabidopsis thalia
963	6	1.8	397	21	AAG45674	Arabidopsis thalia
964	6	1.8	397	22	AAB92573	Human protein sequ
965	6	1.8	398	21	AAG18685	Arabidopsis thalia
966	6	1.8	399	22	ABB60049	Drosophila melanog
967	6	1.8	399	22	ABB69710	Drosophila melanog
968	6	1.8	400	22	ABB68410	Drosophila melanog
969	6	1.8	400	22	ABG17359	Novel human diagno
970	6	1.8	400	22	ABG22434	Novel human diagno
971	6	1.8	402	11	AAR05277	New serine hydroxy
972	6	1.8	402	21	AAG14168	Arabidopsis thalia
973	6	1.8	402	21	AAG18684	Arabidopsis thalia
974	6	1.8	402	21	AAG27429	Arabidopsis thalia
975	6	1.8	403	20	AAW97719	Staphylococcus aur
976	6	1.8	406	20	AAY49152	Amino acid sequenc
977	6	1.8	406	21	AAB27154	H. pylori essentia
978	6	1.8	407	22	AAG91679	C glutamicum prote
979	6	1.8	408	19	AAW71465	Glycosyltransferas
980	6	1.8	408	21	AAY67549	A. orientalis glyc
981	6	1.8	408	22	ABG22973	Novel human diagno
982	6	1.8	409	19	AAY11013	H. pylori ORF hp7e
983	6	1.8	409	19	AAW71464	Glycosyltransferas
984	6	1.8	409	21	AAY57260	A. orientalis glyc
985	6	1.8	410	20	AAY59996	Human endometrium
986	6	1.8	410	22	ABG22423	Novel human diagno
987	6	1.8	412	20	AAY49151	Amino acid sequenc
988	6	1.8	412	22	AAU04815	Micromonospora eve
989	6	1.8	413	20	AAY49139	Amino acid sequenc
990	6	1.8	413	22	ABG08181	Novel human diagno
991	6	1.8	413	22	AAG65755	ATCDPK kinase doma
992	6	1.8	414	21	AAY74313	Neisseria meningit
993	6	1.8	415	22	AAU37000	Staphylococcus aur
994	6	1.8	415	22	AAU37316	Staphylococcus aur
995	6	1.8	416	19	AAW98286	H. pylori GHPO 136
996	6	1.8	416	19	AAW60836	Human LAMP family
997	6	1.8	416	19	AAW50900	S. aureus histidin
998	6	1.8	416	20	AAY29605	Human TSC403 prote
999	6	1.8	416	22	AAU35708	Helicobacter pylor
1000	6	1.8	416	22	AAB94973	Human protein sequ

ALIGNMENTS

```
RESULT   1
AAW36984
ID   AAW36984 standard; Protein; 328 AA.
XX
AC   AAW36984;
XX
DT   21-MAY-1998  (first entry)
XX
DE   E. coli ZipA protein useful in antimicrobial screening.
XX
KW   ZipA protein; antimicrobial; antibiotic; screening.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Sig_peptide
FT   Region          4..13
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          8..13
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          8..20
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          8..24
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          19..24
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          19..26
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          229..233
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          240..247
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          251..254
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          268..271
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT   Region          268..274
FT                   /note= "region of homology with H. influenzae
FT                        ZipA (Claim 16)"
FT
XX
PN   WO9744481-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US08703.
XX
PR   21-MAY-1996;   96US-0651818.
XX
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   De Boer PAJ,  Hale CA;
XX
DR   WPI; 1998-018532/02.
DR   N-PSDB; AAV00469.
XX
PT   Method for screening for antimicrobial compounds - using the zipA
PT   gene of E. coli
XX
PS   Claim 15; Fig 4; 55pp; English.
XX
CC   This protein comprises Escherichia coli ZipA that interacts with
CC   the essential division protein FtsZ.  The amino acid sequence was
CC   deduced from the isolated zipA gene (see AAV00469) and predicts a
CC   mol.wt. of 36.4 kDa.  Database searches did not reveal any known
CC   proteins with significant similarity to ZipA.  A homologue
CC   protein was identified in Haemophilus influenzae Rd.  ZipA
CC   homologues having one or more of 11 claimed regions of homology
CC   are contemplated for use in the invention.  The invention relates
CC   to screening compounds for antimicrobial activity, especially by
CC   using bacterial proteins in vitro to detect compounds that
CC   interfere with cell division.  An expression vector has been
CC   constructed to allow for ZipA protein to be functionally
CC   over-expressed in bacterial cells or other hosts.  The ZipA protein
CC   can be used in a cell-free assay to screen compounds for their
CC   antimicrobial activity, and may also be used in a cellular assay
CC   such as a yeast two-hybrid system.  The antimicrobial compounds
CC   identified by the method are effective against bacteria, and may
CC   also have activity against fungi, mycoplasma and protozoa.
XX
SQ   Sequence   328 AA;

  Query Match             100.0%;  Score 328;  DB 19;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  328;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mmqdlrliliivgaiaiiallvhgfwtsrkerssmfrdrplkrmkskrdddsydedvedd 60
```

```
Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAPH 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 egvgevrvhrvnhapanaqeheaarpspqhqyqppyasaqprqpvqqppeaqvppqhaph 120

Qy     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 paqpvqqpayqpqpeqplqqpvspqvapapqpvhsapqpaqqafqpaepvaapqpepvae 180

Qy     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGEALLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 papvmdkpkrkeaviimnvaahhgselngeallnsiqqagfifgdmniyhrhlspdgsgp 240

Qy     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 alfslanmvkpgtfdpemkdfttpgvtifmqvpsygdelqnfklmlqsaqhiadevggvv 300

Qy     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328
           ||||||||||||||||||||||||||||
Db     301 lddqrrmmtpqklreyqdiirevkdana 328
```

RESULT 2
AAG65926
ID AAG65926 standard; protein; 328 AA.
XX
AC AAG65926;
XX
DT 11-FEB-2002 (first entry)
XX
DE E. coli ZipA protein sequence.
XX
KW ZipA; integral membrane protein; Gram-negative bacteria; antibacterial.
XX
OS Escherichia coli.
XX
PN WO200173436-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-US09826.
XX
PR 28-MAR-2000; 2000US-0536774.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Glasfeld E, Moy FJ, Powers R, Mosyak L, Somers WS;
XX
DR WPI; 2001-656940/75.
XX
PT C-terminal domain of ZipA protein, in solution or crystal form, useful
PT for selection and design of inhibitors, potential antibacterial agents
PT -
XX
PS Disclosure; Fig 1B; 187pp; English.
XX
CC The invention provides a solution containing a C-terminal domain of
CC E. coli ZipA polypeptide. ZipA is an integral membrane protein that is
CC highly conserved among Gram-negative bacteria and essential for
CC development of the septum during bacterial cell division. Crystalline
CC ZipA C-terminal fragment is used for design and selection of inhibitors
CC of ZipA. The inhibitors are potentially useful as antibacterials,
CC effective against Gram-negative species. The present sequence represents
CC an E. coli ZipA protein.
XX
SQ Sequence 328 AA;

Query Match 69.2%; Score 227; DB 22; Length 328;
Best Local Similarity 99.7%; Pred. No. 3.3e-220;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mmqdlrliliivgaiaiiallvhgfwtsrkerssmfrdrplkrmkskrdddsydedvedd 60

Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAPH 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 egvgevrvhrvnhapanaqeheaarpspqhqyqppyasaqprqpvqqppeaqvppqhaph 120

Qy     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 paqpvqqpayqpqpeqplqqpvspqvapapqpvhsapqpaqqafqpaepvaapqpepvae 180

Qy     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGEALLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     181 papvmdkpkrkeaviimnvaahhgselngelllnsiqqagfifgdmniyhrhlspdgsgp 240

Qy     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 alfslanmvkpgtfdpemkdfttpgvtifmqvpsygdelqnfklmlqsaqhiadevggvv 300

Qy     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328
           ||||||||||||||||||||||||||||
Db     301 lddqrrmmtpqklreyqdiirevkdana 328
```

RESULT 3
ABG21781
ID ABG21781 standard; Protein; 864 AA.
XX
AC ABG21781;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #21772.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS85968.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52140; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.

```
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   864 AA;


  Query Match             55.5%;  Score 182;  DB 22;  Length 864;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-174;
  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      29 RKERSSMFRDRPLKRMKSKRDDDSYDEDVEDDEGVGEVRVHRVNHAPANAQEHEAARPSP 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     608 rkerssmfrdrplkrmkskrdddsydedveddegvgevrvhrvnhapanaqeheaarpsp 667

Qy      89 QHQYQPPYASAQPRQPVQQPPEAQVPPQHAPHPAQPVQQPAYQPQPEQPLQQPVSPQVAP 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 qhqyqppyasaqprqpvqqppeaqvppqhaphpaqpvqqpayqpqpeqplqqpvspqvap 727

Qy     149 APQPVHSAPQPAQQAFQPAEPVAAPQPEPVAEPAPVMDKPKRKEAVIIMNVAAHHGSELN 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     728 apqpvhsapqpaqqafqpaepvaapqpepvaepapvmdkpkrkeaviimnvaahhgseln 787

Qy     209 GE 210
           ||
Db     788 ge 789


RESULT   4
AAG65925
ID   AAG65925 standard; protein; 144 AA.
XX
AC   AAG65925;
XX
DT   11-FEB-2002  (first entry)
XX
DE   E. coli ZipA protein C-terminal domain (residues 185-328).
XX
KW   ZipA; integral membrane protein; Gram-negative bacteria; antibacterial.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   Peptide         9..16
FT                   /note= "beta1 strand"
FT   Peptide         25..34
FT                   /note= "alpha 1 helix"
FT   Peptide         37..39
FT                   /note= "beta2 strand"
FT   Peptide         45..48
FT                   /note= "beta3 strand"
FT   Peptide         57..63
FT                   /note= "beta4 strand"
FT   Peptide         81..88
FT                   /note= "beta5 strand"
FT   Peptide         94..112
FT                   /note= "alpha 2 helix"
FT   Peptide         115..117
FT                   /note= "beta6 strand"
FT   Peptide         126..144
FT                   /note= "alpha 3 helix"
XX
PN   WO200173436-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-US09826.
XX
PR   28-MAR-2000; 2000US-0536774.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Glasfeld E,  Moy FJ,  Powers R,  Mosyak L,  Somers WS;
XX
DR   WPI; 2001-656940/75.
XX
PT   C-terminal domain of ZipA protein, in solution or crystal form, useful
PT   for selection and design of inhibitors, potential antibacterial agents
PT   -
XX
PS   Claim 2; Fig 1A; 187pp; English.
XX
CC   The invention provides a solution containing a C-terminal domain of
CC   E. coli ZipA polypeptide. ZipA is an integral membrane protein that is
CC   highly conserved among Gram-negative bacteria and essential for
CC   development of the septum during bacterial cell division. Crystalline
CC   ZipA C-terminal fragment is used for design and selection of inhibitors
CC   of ZipA. The inhibitors are potentially useful as antibacterials,
CC   effective against Gram-negative species. The present sequence represents
CC   an E. coli ZipA protein C-terminal domain fragment.
XX
SQ   Sequence   144 AA;


  Query Match             35.7%;  Score 117;  DB 22;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-109;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     212 LLNSIQQAGFIFGDMNIYHRHLSPDGSGPALFSLANMVKPGTFDPEMKDFTTPGVTIFMQ 271
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 llnsiqqagfifgdmniyhrhlspdgsgpalfslanmvkpgtfdpemkdfttpgvtifmq 87

Qy     272 VPSYGDELQNFKLMLQSAQHIADEVGGVVLDDQRRMMTPQKLREYQDIIREVKDANA 328
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 vpsygdelqnfklmlqsaqhiadevggvvlddqrrmmtpqklreyqdiirevkdana 144


RESULT   5
AAG65927
ID   AAG65927 standard; protein; 328 AA.
XX
AC   AAG65927;
XX
DT   11-FEB-2002  (first entry)
XX
DE   S. typhi ZipA protein sequence.
XX
KW   ZipA; integral membrane protein; Gram-negative bacteria; antibacterial.
XX
OS   Salmonella typhi.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..328
FT                   /note= "residues Xaa are unidentified"
XX
PN   WO200173436-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-US09826.
XX
PR   28-MAR-2000; 2000US-0536774.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Glasfeld E,  Moy FJ,  Powers R,  Mosyak L,  Somers WS;
XX
DR   WPI; 2001-656940/75.
XX
PT   C-terminal domain of ZipA protein, in solution or crystal form, useful
```

```
PT   for selection and design of inhibitors, potential antibacterial agents
PT   -
XX
PS   Disclosure; Fig 1B; 187pp; English.
XX
CC   The invention provides a solution containing a C-terminal domain of
CC   E. coli ZipA polypeptide. ZipA is an integral membrane protein that is
CC   highly conserved among Gram-negative bacteria and essential for
CC   development of the septum during bacterial cell division. Crystalline
CC   ZipA C-terminal fragment is used for design and selection of inhibitors
CC   of ZipA. The inhibitors are potentially useful as antibacterials,
CC   effective against Gram-negative species. Sequences AAG65927-932 represent
CC   ZipA protein sequences from various bacterial species.
XX
SQ   Sequence   328 AA;


  Query Match             6.4%;  Score 21;  DB 22;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     279 LQNFKLMLQSAQHIADEVGGV 299
           |||||||||||||||||||||
Db     279 lqnfklmlqsaqhiadevggv 299


RESULT   6
AAG65928
ID   AAG65928 standard; protein; 328 AA.
XX
AC   AAG65928;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Y. pestis ZipA protein sequence.
XX
KW   ZipA; integral membrane protein; Gram-negative bacteria; antibacterial.
XX
OS   Yersinia pestis.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..328
FT                   /note= "residues Xaa are unidentified"
XX
PN   WO200173436-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-US09826.
XX
PR   28-MAR-2000; 2000US-0536774.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Glasfeld E,  Moy FJ,  Powers R,  Mosyak L,  Somers WS;
XX
DR   WPI; 2001-656940/75.
XX
PT   C-terminal domain of ZipA protein, in solution or crystal form, useful
PT   for selection and design of inhibitors, potential antibacterial agents
PT   -
XX
PS   Disclosure; Fig 1B; 187pp; English.
XX
CC   The invention provides a solution containing a C-terminal domain of
CC   E. coli ZipA polypeptide. ZipA is an integral membrane protein that is
CC   highly conserved among Gram-negative bacteria and essential for
CC   development of the septum during bacterial cell division. Crystalline
CC   ZipA C-terminal fragment is used for design and selection of inhibitors
CC   of ZipA. The inhibitors are potentially useful as antibacterials,
CC   effective against Gram-negative species. Sequences AAG65927-932 represent
CC   ZipA protein sequences from various bacterial species.
XX
SQ   Sequence   328 AA;


  Query Match             3.4%;  Score 11;  DB 22;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     242 LFSLANMVKPG 252
           ||||||||||| 
Db     239 lfslanmvkpg 249


RESULT   7
AAW81571
ID   AAW81571 standard; Protein; 522 AA.
XX
AC   AAW81571;
XX
DT   01-MAR-1999  (first entry)
XX
DE   Mus dunni endogenous virus Gag protein.
XX
KW   MDEV; retrovirus; packaging cell line; gene transfer; gene therapy;
KW   vector; Gag protein.
XX
OS   Mus dunni endogenous virus.
XX
PN   WO9850538-A1.
XX
PD   12-NOV-1998.
XX
PF   08-MAY-1998;   98WO-US09452.
XX
PR   08-MAY-1998;   98US-0075272.
PR   09-MAY-1997;   97US-0046140.
XX
PA   (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI   Bonham L,  Miller AD,  Wolgamot G;
XX
DR   WPI; 1999-034718/03.
DR   N-PSDB; AAV69750.
XX
PT   New retroviral packaging cells - containing Mus dunni endogenous
PT   virus sequences to target cells, retrovirus gag and pol genes and a
PT   heterologous gene of interest.
XX
PS   Disclosure; Page 67-68; 85pp; English.
XX
CC   This is the amino acid sequence of the Gag protein of
CC   Mus dunni endogenous virus (MDEV), as deduced from the MDEV
CC   nucleotide sequence (see AAV69750). A cultured packaging cell is
CC   claimed which produces a replication-defective retroviral vector
CC   (RDRV) particle, where the packaging cell is a vertebrate cell
CC   capable of expressing and assembling retroviral proteins,
CC   comprising: (a) a first vector encoding a retroviral envelope
CC   protein having amino acid residues MDEV that direct binding of the
CC   retroviral particle to MDEV retroviral receptors on a target cell;
CC   and (b) a second vector encoding retrovirus Gag and Pol proteins,
CC   where upon expression of the vectors in the packaging cell in the
CC   presence of a vector having a sequence of a heterologous gene of
CC   interest, a replication-defective retroviral particle is produced
CC   that binds to MDEV receptors of target cells. Also claimed are:
CC   (1) a cultured packaging cell for producing a RDRV particle; (2)
CC   methods for producing a RDRV particle comprising a heterologous
CC   gene of interest; (3) cultured packaging cell line PD223; and (4) a
CC   RDRV produced by a method as in (2). The MDEV receptor is present
CC   on a variety of cells rendering MDEV pseudotype packaging cells
CC   useful in methods of mammalian and particularly human gene transfer
CC   for gene therapy. The MDEV packaging cells are a stable and
CC   reproducible source of retroviral particles. Clones may be
CC   isolated from these populations that produce high titre virus. The
CC   packaging cell lines may be selected and cloned for other desirable
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```
CC   properties, such as stability of in vivo growth, lack of production
CC   of helper virus, lack of reinfection by viral particles packaged in
CC   the cell, stability from genetic rearrangement and recombinational
CC   events, resistance to complement lysis, and improved ability to
CC   infect cells from higher mammals.
XX
SQ   Sequence   522 AA;


  Query Match             2.7%;  Score 9;  DB 20;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     169 PVAAPQPEP 177
           |||||||||
Db     156 pvaapqpep 164


RESULT   8
AAW81570
ID   AAW81570 standard; Protein; 622 AA.
XX
AC   AAW81570;
XX
DT   01-MAR-1999  (first entry)
XX
DE   Mus dunni endogenous virus Gag protein (glycosylated).
XX
KW   MDEV; retrovirus; packaging cell line; gene transfer; gene therapy;
KW   vector; Gag protein.
XX
OS   Mus dunni endogenous virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "encoded by CTG"
XX
PN   WO9850538-A1.
XX
PD   12-NOV-1998.
XX
PF   08-MAY-1998;   98WO-US09452.
XX
PR   08-MAY-1998;   98US-0075272.
PR   09-MAY-1997;   97US-0046140.
XX
PA   (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI   Bonham L,  Miller AD,  Wolgamot G;
XX
DR   WPI; 1999-034718/03.
DR   N-PSDB; AAV69750.
XX
PT   New retroviral packaging cells - containing Mus dunni endogenous
PT   virus sequences to target cells, retrovirus gag and pol genes and a
PT   heterologous gene of interest.
XX
PS   Disclosure; Page 65-66; 85pp; English.
XX
CC   This is the amino acid sequence of the glycosylated Gag protein of
CC   Mus dunni endogenous virus (MDEV), as deduced from the MDEV
CC   nucleotide sequence (see AAV69750).  A cultured packaging cell is
CC   claimed which produces a replication-defective retroviral vector
CC   (RDRV) particle, where the packaging cell is a vertebrate cell
CC   capable of expressing and assembling retroviral proteins,
CC   comprising: (a) a first vector encoding a retroviral envelope
CC   protein having amino acid residues MDEV that direct binding of the
CC   retroviral particle to MDEV retroviral receptors on a target cell;
CC   and (b) a second vector encoding retrovirus Gag and Pol proteins,
CC   where upon expression of the vectors in the packaging cell in the
CC   presence of a vector having a sequence of a heterologous gene of
CC   interest, a replication-defective retroviral particle is produced
CC   that binds to MDEV receptors of target cells.  Also claimed are:
CC   (1) a cultured packaging cell for producing a RDRV particle; (2)
CC   methods for producing a RDRV particle comprising a heterologous
CC   gene of interest; (3) cultured packaging cell line PD223; and (4) a
CC   RDRV produced by a method as in (2).  The MDEV receptor is present
CC   on a variety of cells rendering MDEV pseudotype packaging cells
CC   useful in methods of mammalian and particularly human gene transfer
CC   for gene therapy.  The MDEV packaging cells are a stable and
CC   reproducible source of retroviral particles.  Clones may be
CC   isolated from these populations that produce high titre virus.  The
CC   packaging cell lines may be selected and cloned for other desirable
CC   properties, such as stability of in vivo growth, lack of production
CC   of helper virus, lack of reinfection by viral particles packaged in
CC   the cell, stability from genetic rearrangement and recombinational
CC   events, resistance to complement lysis, and improved ability to
CC   infect cells from higher mammals.
XX
SQ   Sequence   622 AA;


  Query Match             2.7%;  Score 9;  DB 20;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     169 PVAAPQPEP 177
           |||||||||
Db     256 pvaapqpep 264


RESULT   9
AAO03175
ID   AAO03175 standard; Protein; 36 AA.
XX
AC   AAO03175;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 17067.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI83106.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 17067; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
```

CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 36 AA;

Query Match 2.4%; Score 8; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 SLANMVKP 251
||||||||
Db 28 slanmvkp 35

RESULT 10
AAM87430
ID AAM87430 standard; Protein; 41 AA.
XX
AC AAM87430;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:15023.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK60211.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 11; SEQ ID NO 15023; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 41 AA;

Query Match 2.4%; Score 8; DB 22; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 SLANMVKP 251
||||||||
Db 29 slanmvkp 36

RESULT 11
AAO13330
ID AAO13330 standard; Protein; 42 AA.
XX
AC AAO13330;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 27222.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI93261.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 27222; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 42 AA;

Query Match 2.4%; Score 8; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 SLANMVKP 251
||||||||
Db 32 slanmvkp 39

RESULT 12
AAO13438
ID AAO13438 standard; Protein; 44 AA.
XX

```
AC   AAO13438;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 27330.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI93369.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 27330; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   44 AA;

  Query Match             2.4%;  Score 8;  DB 22;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     244 SLANMVKP 251
           ||||||||
Db      34 slanmvkp 41


RESULT  13
ABG05119
ID   ABG05119 standard; Protein; 45 AA.
XX
AC   ABG05119;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #5110.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS69306.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 35478; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   45 AA;

  Query Match             2.4%;  Score 8;  DB 22;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     244 SLANMVKP 251
           ||||||||
Db      35 slanmvkp 42


RESULT  14
AAO13238
ID   AAO13238 standard; Protein; 45 AA.
XX
AC   AAO13238;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 27130.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
```

KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI93169.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing.
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 27130; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 45 AA;

Query Match 2.4%; Score 8; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 SLANMVKP 251
||||||||
Db 34 slanmvkp 41

RESULT 15
AAO02012
ID AAO02012 standard; Protein; 46 AA.
XX
AC AAO02012;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 15904.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI81943.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 15904; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 46 AA;

Query Match 2.4%; Score 8; DB 22; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 SLANMVKP 251
||||||||
Db 39 slanmvkp 46

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 25, 2002, 09:50:06 ; Search time 13.2 Seconds
(without alignments)
606.939 Million cell updates/sec

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Perfect score: 328
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Gapop 60.0 , Gapext 60.0

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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282	6	1.8	3418	2	US-08-603-753D-4	Sequence 4, Appli
283	6	1.8	3418	3	US-09-044-946-2	Sequence 2, Appli
284	6	1.8	3418	3	US-08-755-587-44	Sequence 44, Appl
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297	5	1.5	9	2	US-08-986-948-9	Sequence 9, Appli
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369	5	1.5	18	3	US-08-940-093-226	Sequence 226, App
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422	5	1.5	31	1	US-08-190-802A-160	Sequence 160, App
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563	5	1.5	42	4	US-09-005-215-20	Sequence 20, Appl
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694	5	1.5	73	4	US-08-475-411A-110	Sequence 110, App
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713	5	1.5	77	2	US-08-798-143-9	Sequence 9, Appli
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771	5	1.5	97	4	US-08-478-029A-99	Sequence 99, Appl
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775	5	1.5	97	6	5223482-8	Patent No. 5223482
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833	5	1.5	106	2	US-08-583-118-3	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 2, Application US/08651818A
; Patent No. 5948889
;  GENERAL INFORMATION:
;    APPLICANT:  de Boer, Piet A.J.
;    APPLICANT:  Hale, Cynthia A.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR SCREENING
;    TITLE OF INVENTION:  ANTIMICROBIALS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/651,818A
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  CASE-02249
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-651-818A-2

  Query Match           100.0%;  Score 328;  DB 2;  Length 328;
  Best Local Similarity  100.0%;  Pred. No. 0;
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;    APPLICANT:  de Boer, Piet A.J.
;    APPLICANT:  Hale, Cynthia A.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR SCREENING
;    TITLE OF INVENTION:  ANTIMICROBIALS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/184,826
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  CASE-02249
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-184-826-2

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; Patent No. 6136598
;  GENERAL INFORMATION:
;    APPLICANT:  MILLER, A. DUSTY
;    APPLICANT:  WOLGAMOT, GREG
;    APPLICANT:  BONHAM, LYNN
;    TITLE OF INVENTION:  MUS DUNNI ENDOGENOUS RETROVIRAL
;    TITLE OF INVENTION:  PACKAGING CELL LINES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/075,272
;      FILING DATE:  08-MAY-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/046,140
;      FILING DATE:  09-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  14538A-003710
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  522 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-075-272-3


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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     169 PVAAPQPEP 177
           |||||||||
Db     156 PVAAPQPEP 164


RESULT   4
US-09-075-272-2
; Sequence 2, Application US/09075272
; Patent No. 6136598
;  GENERAL INFORMATION:
;    APPLICANT:  MILLER, A. DUSTY
;    APPLICANT:  WOLGAMOT, GREG
;    APPLICANT:  BONHAM, LYNN
;    TITLE OF INVENTION:  MUS DUNNI ENDOGENOUS RETROVIRAL
;    TITLE OF INVENTION:  PACKAGING CELL LINES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/075,272
;      FILING DATE:  08-MAY-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/046,140
;      FILING DATE:  09-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  14538A-003710
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  622 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-075-272-2


  Query Match             2.7%;  Score 9;  DB 4;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     169 PVAAPQPEP 177
           |||||||||
Db     256 PVAAPQPEP 264


RESULT   5
US-09-172-045-2
; Sequence 2, Application US/09172045
; Patent No. 6277594
; GENERAL INFORMATION:
;  APPLICANT: Mikoshiba, Katsuhiko
;  APPLICANT: Aruga, Jun
;  APPLICANT: Nagai, Takeharu
;  APPLICANT: Nakata, Katsunori
```

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;  TITLE OF INVENTION: Neurogenesis Inducing Gene
;  FILE REFERENCE: Hiraki-03497
;  CURRENT APPLICATION NUMBER: US/09/172,045
;  CURRENT FILING DATE: 1998-10-08
;  EARLIER APPLICATION NUMBER: JP98/86979
;  EARLIER FILING DATE: 1998-03-31
;  EARLIER APPLICATION NUMBER: JP98/121456
;  EARLIER FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 441
;    TYPE: PRT
;    ORGANISM: Xenopus laevis
US-09-172-045-2


  Query Match             2.4%;  Score 8;  DB 4;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 8.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    197 MNVAAHHG 204
          ||||||||
Db    199 MNVAAHHG 206


RESULT   6
US-08-374-483-4
; Sequence 4, Application US/08374483
; Patent No. 5880102
;  GENERAL INFORMATION:
;    APPLICANT:  GEORGE, SAMUEL E.
;    APPLICANT:  BLAZING, MICHAEL A.
;    TITLE OF INVENTION:  ADENOVIRAL VECTOR SYSTEM
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,483
;      FILING DATE:  17-JAN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARY J.
;      REGISTRATION NUMBER:  32,955
;      REFERENCE/DOCKET NUMBER:  1579-83
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4000
;      TELEFAX:  (703) 816-4100
;      TELEX:  200797 NIXN UR
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1015 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-374-483-4


  Query Match             2.4%;  Score 8;  DB 2;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    176 EPVAEPAP 183
          ||||||||
Db    953 EPVAEPAP 960


RESULT   7
US-08-374-483-7
; Sequence 7, Application US/08374483
; Patent No. 5880102
;  GENERAL INFORMATION:
;    APPLICANT:  GEORGE, SAMUEL E.
;    APPLICANT:  BLAZING, MICHAEL A.
;    TITLE OF INVENTION:  ADENOVIRAL VECTOR SYSTEM
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,483
;      FILING DATE:  17-JAN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARY J.
;      REGISTRATION NUMBER:  32,955
;      REFERENCE/DOCKET NUMBER:  1579-83
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4000
;      TELEFAX:  (703) 816-4100
;      TELEX:  200797 NIXN UR
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1015 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-374-483-7


  Query Match             2.4%;  Score 8;  DB 2;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    176 EPVAEPAP 183
          ||||||||
Db    953 EPVAEPAP 960


RESULT   8
US-08-818-112-142
; Sequence 142, Application US/08818112
; Patent No. 6290969
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonio
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;    TITLE OF INVENTION:  AND DIAGNOSIS OF TUBERCULOSIS
;    NUMBER OF SEQUENCES:  153
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,112
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.411C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  142:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-818-112-142


  Query Match             2.1%;  Score 7;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     146 VAPAPQP 152
           |||||||
Db     244 VAPAPQP 250


RESULT  9
US-08-818-111-137
; Sequence 137, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,111
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  137:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-818-111-137


  Query Match             2.1%;  Score 7;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     146 VAPAPQP 152
           |||||||
Db     244 VAPAPQP 250


RESULT  10
US-09-056-556-142
; Sequence 142, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE PREVENTION AND            TRE
;    NUMBER OF SEQUENCES:  241
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,556
;      FILING DATE:  07-APR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.457
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  142:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-056-556-142


  Query Match             2.1%;  Score 7;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     146 VAPAPQP 152
           |||||||
```

```
Db    244 VAPAPQP 250


RESULT  11
US-08-892-880-3
; Sequence 3, Application US/08892880
; Patent No. 5942417
;  GENERAL INFORMATION:
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER L.
;    APPLICANT:  DILLON, PATRICK J.
;    TITLE OF INVENTION:  CD44-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,880
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/021,762
;      FILING DATE:  15-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0490001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-892-880-3


  Query Match             2.1%;  Score 7;  DB 2;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     205 SELNGEA 211
           |||||||
Db     296 SELNGEA 302


RESULT  12
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-07-946-497-7


  Query Match             2.1%;  Score 7;  DB 1;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     205 SELNGEA 211
           |||||||
Db     318 SELNGEA 324


RESULT  13
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,322
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/946,497
;      FILING DATE:  09-NOV-1992
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-08-483-322-7


  Query Match             2.1%;  Score 7;  DB 1;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     205 SELNGEA 211
           |||||||
Db     318 SELNGEA 324


RESULT  14
US-08-478-882-7
; Sequence 7, Application US/08478882
; Patent No. 5885575
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,882
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-08-478-882-7


  Query Match             2.1%;  Score 7;  DB 2;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     205 SELNGEA 211
           |||||||
Db     318 SELNGEA 324


RESULT  15
US-07-946-497-2
; Sequence 2, Application US/07946497
; Patent No. 5506119
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  503 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-946-497-2


  Query Match             2.1%;  Score 7;  DB 1;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     205 SELNGEA 211
           |||||||
Db     458 SELNGEA 464


Search completed: September 25, 2002, 09:52:55
Job time: 169 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 25, 2002, 09:50:51 ; Search time 17.78 Seconds
(without alignments)
1772.627 Million cell updates/sec

Title: US-09-184-826-2
Perfect score: 328
Sequence: 1 MMQDLRLILIIVGAIAIIAL.....TPQKLREYQDIIREVKDANA 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	227	69.2	328	2	C65015	hypothetical prote
2	119	36.3	332	2	D91039	cell division prot
3	117	35.7	328	2	G85883	cell division prot
4	54	16.5	328	2	AB0810	cell division prot
5	11	3.4	328	2	AG0363	probable cell divi
6	9	2.7	137	2	T22308	hypothetical prote
7	8	2.4	130	2	D84353	hypothetical prote
8	8	2.4	339	2	S37920	MBR1 protein precu
9	8	2.4	405	2	AE0990	probable membrane
10	8	2.4	419	1	S47692	hypothetical 43.8K
11	8	2.4	419	2	B91169	probable transport
12	8	2.4	419	2	B86015	probable transport
13	8	2.4	512	2	G86773	citrate (pro-3S)-l
14	8	2.4	912	2	B97566	hypothetical prote
15	8	2.4	1008	2	AH2786	conserved hypothet
16	8	2.4	2485	1	H71621	serine/threonine-s
17	7	2.1	49	2	S23290	light-harvesting p
18	7	2.1	82	2	G84456	hypothetical prote
19	7	2.1	176	2	T26212	hypothetical prote
20	7	2.1	186	2	T31951	hypothetical prote
21	7	2.1	202	2	T15874	hypothetical prote
22	7	2.1	206	2	A84236	30S ribosomal prot
23	7	2.1	212	2	E81669	conserved hypothet
24	7	2.1	213	2	E71511	hypothetical prote
25	7	2.1	246	2	A70124	hypothetical prote
26	7	2.1	250	2	T14000	aquaporin TIP7 - c
27	7	2.1	253	2	AC0654	hypothetical oxido
28	7	2.1	271	2	D71103	probable homoserin
29	7	2.1	272	2	E83363	hypothetical prote
30	7	2.1	278	1	TPHUTW	troponin T, slow s
31	7	2.1	285	2	C98105	hypothetical prote
32	7	2.1	285	2	B95241	conserved hypothet
33	7	2.1	288	2	E64202	fructose-bisphosph
34	7	2.1	289	2	E83454	cell division prot
35	7	2.1	290	2	B83924	hypothetical prote
36	7	2.1	290	2	T48880	beta-lactamase (EC
37	7	2.1	291	2	E82258	cell division prot
38	7	2.1	304	2	T42521	probable UTP--gluc
39	7	2.1	312	2	C82208	siroheme synthase
40	7	2.1	328	2	D84030	delta-aminolevulin
41	7	2.1	340	2	A72600	probable dehydroge
42	7	2.1	356	2	JQ2352	glycoprotein I - t
43	7	2.1	356	2	G82523	endo-1,4-beta-gluc
44	7	2.1	358	2	G81822	translation releas
45	7	2.1	358	2	G81053	translation releas
46	7	2.1	362	2	A35616	T-cell surface gly
47	7	2.1	363	2	A37009	CD44 homolog membr
48	7	2.1	365	2	A34424	CD44 membrane glyc
49	7	2.1	372	2	T38192	hypothetical prote
50	7	2.1	380	2	G86656	ABC transporter pe
51	7	2.1	396	2	B75186	hypothetical prote
52	7	2.1	404	2	B89819	pyrimidine nucleos
53	7	2.1	455	2	A87913	protein B0205.10 [
54	7	2.1	460	2	S01508	NADH dehydrogenase
55	7	2.1	461	2	T11800	NADH dehydrogenase
56	7	2.1	482	2	A39132	anthranilate synth
57	7	2.1	485	2	T19394	hypothetical prote
58	7	2.1	487	1	QQECRS	ygjE protein - Esc
59	7	2.1	502	2	H75290	hypothetical prote
60	7	2.1	502	2	A70988	hypothetical prote
61	7	2.1	503	2	B38745	cell adhesion mole
62	7	2.1	506	2	T40935	probable utp--gluc
63	7	2.1	525	2	JN0443	transcription init
64	7	2.1	548	2	E70546	hypothetical prote
65	7	2.1	562	2	T15131	hypothetical prote
66	7	2.1	583	2	C97610	cell division prot
67	7	2.1	583	2	AG2832	cell division prot
68	7	2.1	609	2	G87496	peptidase, M23/M37
69	7	2.1	615	2	T29550	hypothetical prote
70	7	2.1	693	2	C87575	sensor histidine k
71	7	2.1	736	2	A86171	hypothetical prote
72	7	2.1	745	2	G72453	hypothetical prote
73	7	2.1	762	2	H87302	chemotaxis protein
74	7	2.1	802	2	S42518	PML protein, splic
75	7	2.1	802	2	S44382	PML protein, splic
76	7	2.1	874	2	T34922	phosphoenolpyruvat
77	7	2.1	880	2	D89756	protein T23E7.2b [
78	7	2.1	899	2	C95339	hypothetical prote
79	7	2.1	1006	2	JC5526	kinase-defective E
80	7	2.1	1018	1	S73720	cytadherence acces
81	7	2.1	1073	2	S56220	probable membrane
82	7	2.1	1242	2	T20739	hypothetical prote
83	7	2.1	1420	2	T37781	probable cytoskele
84	7	2.1	1448	2	F83237	probable ATP-depen
85	7	2.1	1782	2	S45289	vitellogenin precu
86	7	2.1	2777	2	D96746	hypothetical prote
87	7	2.1	6359	2	T31679	bacitracin synthet
88	6	1.8	16	2	PH0754	T-cell receptor be
89	6	1.8	26	2	C33174	avematin - oat (fr
90	6	1.8	39	2	T12912	hypothetical prote
91	6	1.8	41	2	T07236	photosystem I psbJ
92	6	1.8	41	2	H64039	hypothetical prote
93	6	1.8	44	2	B38075	N-acetylgalactosam
94	6	1.8	47	2	AE3429	hypothetical prote
95	6	1.8	53	2	F90763	hypothetical prote
96	6	1.8	53	2	D82553	hypothetical prote
97	6	1.8	57	2	PN0624	alpha-internexin -
98	6	1.8	57	2	E82733	hypothetical prote
99	6	1.8	70	2	A83982	hypothetical prote
100	6	1.8	71	2	S45608	light-harvesting p
101	6	1.8	73	2	G95106	hypothetical prote
102	6	1.8	75	2	AG1731	hypothetical prote

103	6	1.8	79	2	AC0509	oxaloacetate decar
104	6	1.8	80	2	AF0909	oxaloacetate decar
105	6	1.8	82	2	E87465	host factor-I prot
106	6	1.8	90	2	A38934	porphobilinogen sy
107	6	1.8	90	2	G75509	hypothetical prote
108	6	1.8	91	2	T17968	hypothetical prote
109	6	1.8	92	2	D72223	conserved hypothet
110	6	1.8	92	2	S21307	hypothetical prote
111	6	1.8	92	2	E72581	hypothetical prote
112	6	1.8	93	2	S72254	ribosomal protein
113	6	1.8	94	2	B82847	hypothetical prote
114	6	1.8	95	1	FELV	ferredoxin [2Fe-2S
115	6	1.8	97	2	F70939	hypothetical prote
116	6	1.8	98	2	S69086	cystatin A - bovin
117	6	1.8	98	2	T44883	hypothetical prote
118	6	1.8	98	2	S53467	hypothetical prote
119	6	1.8	100	2	T36231	probable dehydroge
120	6	1.8	100	2	G81749	hypothetical prote
121	6	1.8	100	2	C72690	hypothetical prote
122	6	1.8	100	2	E91280	cytochrome b(562)
123	6	1.8	100	2	E86121	cytochrome b (562)
124	6	1.8	100	2	AG0279	acetolactate synth
125	6	1.8	101	2	A36869	probable export pr
126	6	1.8	101	2	F90964	flagellar protein
127	6	1.8	101	2	F85812	flagelar biosynthe
128	6	1.8	103	2	AF0031	probable membrane
129	6	1.8	103	2	A82694	hypothetical prote
130	6	1.8	104	2	A60094	neurofilament-M ho
131	6	1.8	107	2	T44532	hypothetical prote
132	6	1.8	108	2	G84522	similar to gibbere
133	6	1.8	110	2	B69403	hypothetical prote
134	6	1.8	110	2	G72597	hypothetical prote
135	6	1.8	111	2	A71507	probable L22 ribos
136	6	1.8	112	2	G72645	hypothetical prote
137	6	1.8	112	2	H95198	hypothetical prote
138	6	1.8	117	2	C69969	hypothetical prote
139	6	1.8	117	2	F98065	hypothetical prote
140	6	1.8	118	2	F75445	hypothetical prote
141	6	1.8	122	2	G69840	conserved hypothet
142	6	1.8	124	2	A47582	B-cell growth fact
143	6	1.8	126	2	I61260	synapsin II - mous
144	6	1.8	127	2	AI0329	conserved hypothet
145	6	1.8	127	2	F81026	conserved hypothet
146	6	1.8	127	2	F95968	hypothetical prote
147	6	1.8	128	1	CBEC62	cytochrome b562 pr
148	6	1.8	128	2	AF0449	probable cytochrom
149	6	1.8	128	2	AF1056	soluble cytochrome
150	6	1.8	128	2	T32947	hypothetical prote
151	6	1.8	129	2	AH1458	B. subtilis YabA p
152	6	1.8	130	2	AE2472	hypothetical prote
153	6	1.8	131	2	AH0348	probable membrane
154	6	1.8	132	2	T18095	hypothetical prote
155	6	1.8	133	1	F45345	trans-regulatory s
156	6	1.8	134	2	E81133	hypothetical prote
157	6	1.8	135	2	E70585	probable transcrip
158	6	1.8	136	2	B96504	protein F9C16.21 [
159	6	1.8	136	2	H83312	probable type II s
160	6	1.8	138	1	DMPG	desmin - pig (frag
161	6	1.8	138	2	E95917	hypothetical proli
162	6	1.8	139	2	A64412	hypothetical prote
163	6	1.8	139	2	H81886	hypothetical prote
164	6	1.8	139	2	H81812	duplicated hypothe
165	6	1.8	139	2	S42605	hypothetical prote
166	6	1.8	140	2	C70223	conserved hypothet
167	6	1.8	142	1	WMAD19	early E1B 17K prot
168	6	1.8	142	2	AB0940	probable membrane
169	6	1.8	143	2	H71641	hypothetical prote
170	6	1.8	143	2	H83894	hypothetical prote
171	6	1.8	143	2	B53045	translation initia
172	6	1.8	144	2	G86293	40S ribosomal prot
173	6	1.8	144	2	C98131	hypothetical prote
174	6	1.8	144	2	AF3156	hypothetical prote
175	6	1.8	145	2	C84370	cytochrome c oxida
176	6	1.8	146	2	AI0450	conserved hypothet
177	6	1.8	147	2	A70462	ribosomal protein
178	6	1.8	147	2	F72730	yhcV homolog APE03
179	6	1.8	148	2	T03982	5-epi-aristolochen
180	6	1.8	148	2	T31040	conserved hypothet
181	6	1.8	148	2	H75096	hypothetical prote
182	6	1.8	149	2	E90655	hypothetical prote
183	6	1.8	151	2	F82427	hypothetical prote
184	6	1.8	151	2	T10768	latex allergen Hev
185	6	1.8	151	2	F85506	hypothetical prote
186	6	1.8	156	2	E64084	kdtB protein - Hae
187	6	1.8	156	2	T20267	hypothetical prote
188	6	1.8	156	2	T50413	hypothetical prote
189	6	1.8	157	2	C71814	lipopolysaccharide
190	6	1.8	157	2	C64704	lipopolysaccharide
191	6	1.8	158	2	G81347	3-deoxy-D-manno-oc
192	6	1.8	159	2	JU0468	kdtB protein - Esc
193	6	1.8	159	2	E91192	phosphopantetheine
194	6	1.8	159	2	A83600	phosphopantetheine
195	6	1.8	159	2	F86039	probable enzyme of
196	6	1.8	159	2	AF0007	pantetheine-phosph
197	6	1.8	159	2	AH0971	pantetheine-phosph
198	6	1.8	159	2	T51520	hypothetical prote
199	6	1.8	160	1	S14574	globin C precursor
200	6	1.8	160	2	AD1331	phosphopantetheine
201	6	1.8	160	2	S65978	spore coat protein
202	6	1.8	160	2	E95882	hypothetical trans
203	6	1.8	160	2	G90168	conserved hypothet
204	6	1.8	161	1	JT0292	hemoglobin VIIB-5/
205	6	1.8	161	1	JT0349	hemoglobin VIIB-5
206	6	1.8	161	1	A30477	hemoglobin VIIB-6
207	6	1.8	161	1	S04499	hemoglobin VIIB-8
208	6	1.8	161	1	S04500	hemoglobin VIIB-9
209	6	1.8	161	1	S14576	globin E precursor
210	6	1.8	161	2	A95049	hypothetical prote
211	6	1.8	161	2	G97919	acetyl-CoA carboxy
212	6	1.8	161	2	B70323	lipopolysaccharide
213	6	1.8	161	2	AD1702	phosphopantetheine
214	6	1.8	161	2	AF0013	S-adenosylmethioni
215	6	1.8	162	2	C82738	lipopolysaccharide
216	6	1.8	162	2	D98020	conserved hypothet
217	6	1.8	162	2	H70927	probable rpsP prot
218	6	1.8	163	1	S21632	hemoglobin Z precu
219	6	1.8	163	2	D87445	hypothetical prote
220	6	1.8	163	2	T25347	hypothetical prote
221	6	1.8	163	2	AD0462	probable exported
222	6	1.8	164	2	H82347	lipopolysaccharide
223	6	1.8	164	2	AI2183	hypothetical prote
224	6	1.8	165	2	S44302	single-stranded DN
225	6	1.8	165	2	H84997	hypothetical prote
226	6	1.8	166	2	AD1744	low temperature re
227	6	1.8	166	2	AF1374	B. subtilis YutG p
228	6	1.8	167	2	D82561	probable signal pe
229	6	1.8	168	2	AF2620	conserved hypothet
230	6	1.8	168	2	AG2257	hypothetical prote
231	6	1.8	169	2	I55299	cytochrome P450 PB
232	6	1.8	169	2	S72166	lipopolysaccharide
233	6	1.8	169	2	H84077	low temperature re
234	6	1.8	170	2	E86341	F9H16.13 protein -
235	6	1.8	172	2	T12202	probable cdc2-like
236	6	1.8	174	2	JC1294	papE fimbrial prot
237	6	1.8	174	2	T21945	hypothetical prote
238	6	1.8	175	2	JE0350	Anterior gradient-
239	6	1.8	175	2	D86180	hypothetical prote
240	6	1.8	176	2	JT0616	cystatin-related p
241	6	1.8	179	2	D64591	adenine phosphorib
242	6	1.8	179	2	H71920	adenine phosphorib
243	6	1.8	180	2	F97402	hypothetical prote
244	6	1.8	180	2	C72676	hypothetical prote
245	6	1.8	180	2	S06616	chorion protein s1
246	6	1.8	181	2	S23521	oleosin - common s
247	6	1.8	181	2	E83436	probable oxidase P
248	6	1.8	183	2	AI0710	probable nitroredu

249	6	1.8	184	2	S78091	endocuticular prot
250	6	1.8	184	2	A70149	transcription anti
251	6	1.8	185	2	T25891	hypothetical prote
252	6	1.8	185	2	I40490	hypothetical prote
253	6	1.8	187	2	B86704	hypothetical prote
254	6	1.8	189	2	H83281	conserved hypothet
255	6	1.8	190	2	AG0579	antimicrobial pept
256	6	1.8	190	2	C90260	hypothetical prote
257	6	1.8	191	2	A72536	hypothetical prote
258	6	1.8	191	2	A82225	hypothetical prote
259	6	1.8	191	2	JQ1919	hypothetical 21.3K
260	6	1.8	191	2	AE0412	probable 2'-5' RNA
261	6	1.8	193	2	JC2439	iron sulfur protei
262	6	1.8	193	2	AD2402	hypothetical prote
263	6	1.8	194	2	S21859	hypothetical prote
264	6	1.8	197	2	F83846	spore maturation p
265	6	1.8	197	2	C90671	hypothetical prote
266	6	1.8	197	2	G85521	hypothetical prote
267	6	1.8	197	2	F70832	probable membrane
268	6	1.8	197	2	B81720	conserved hypothet
269	6	1.8	197	2	T35766	hypothetical prote
270	6	1.8	198	2	A96520	hypothetical prote
271	6	1.8	198	2	AG2530	hypothetical prote
272	6	1.8	200	1	QQBE27	BZLF1 protein - hu
273	6	1.8	200	2	E64756	membrane protein y
274	6	1.8	200	2	G69307	polyferredoxin (mv
275	6	1.8	200	2	E87497	hypothetical prote
276	6	1.8	201	2	AD2503	hypothetical prote
277	6	1.8	201	2	AI3484	low molecular weig
278	6	1.8	202	2	T11895	NADH dehydrogenase
279	6	1.8	203	2	E81449	hypothetical prote
280	6	1.8	203	2	T24537	hypothetical prote
281	6	1.8	204	2	S63655	NADH dehydrogenase
282	6	1.8	205	1	ASLJIK	nef protein - simi
283	6	1.8	205	2	C75155	methlytransferase
284	6	1.8	208	2	T47735	hypothetical prote
285	6	1.8	208	2	C82742	transcription regu
286	6	1.8	211	2	S28046	TUB8 protein - pot
287	6	1.8	213	2	S25647	ookinete surface p
288	6	1.8	213	2	E83386	hypothetical prote
289	6	1.8	213	2	JC1152	hypothetical prote
290	6	1.8	215	2	S78275	ribosomal protein
291	6	1.8	215	2	D84382	hypothetical prote
292	6	1.8	215	2	D75342	conserved hypothet
293	6	1.8	216	2	B96946	amino acid (glutam
294	6	1.8	216	2	A37762	hypothetical prote
295	6	1.8	217	2	D95162	hypothetical prote
296	6	1.8	217	2	C98028	phosphate transpor
297	6	1.8	217	2	C86839	phosphate transpor
298	6	1.8	218	2	T49841	hypothetical prote
299	6	1.8	219	2	B43772	neurofilament trip
300	6	1.8	219	2	E75219	hypothetical prote
301	6	1.8	219	2	E87673	conserved hypothet
302	6	1.8	221	2	T45044	hypothetical prote
303	6	1.8	221	2	AI3631	hypothetical prote
304	6	1.8	222	2	T34060	hypothetical prote
305	6	1.8	222	2	A49995	salt-mediated kill
306	6	1.8	223	2	A87483	hypothetical prote
307	6	1.8	224	2	T14841	phytochrome 22 - N
308	6	1.8	224	2	T37156	probable transcrip
309	6	1.8	225	2	C90591	beta-phosphoglucom
310	6	1.8	226	2	T30695	probable uracil DN
311	6	1.8	227	2	G70555	hypothetical prote
312	6	1.8	227	2	AC0359	probable membrane
313	6	1.8	228	2	T16678	hypothetical prote
314	6	1.8	228	2	H69025	hypothetical prote
315	6	1.8	228	2	F87670	SurF1 family prote
316	6	1.8	228	2	B84178	TRK potassium upta
317	6	1.8	228	2	A96918	probable enzyme wi
318	6	1.8	229	2	T27466	hypothetical prote
319	6	1.8	230	2	T15381	hypothetical prote
320	6	1.8	230	2	G82579	conserved hypothet
321	6	1.8	231	2	C83300	hypothetical prote
322	6	1.8	232	2	D71218	hypothetical prote
323	6	1.8	232	2	G89025	protein F13A2.8 [i
324	6	1.8	232	2	T17553	hypothetical prote
325	6	1.8	232	2	AB1908	hypothetical prote
326	6	1.8	233	2	AG2538	hypothetical prote
327	6	1.8	234	2	T00931	hypothetical prote
328	6	1.8	234	2	AH3335	probable membrane-
329	6	1.8	237	1	B42371	regulatory protein
330	6	1.8	237	2	D95113	O-methyltransferas
331	6	1.8	237	2	T30028	hypothetical prote
332	6	1.8	237	2	C97982	conserved hypothet
333	6	1.8	238	2	A84059	16S pseudouridylat
334	6	1.8	238	2	C70321	Rieske iron-sulfur
335	6	1.8	239	2	F96908	uncharacterized co
336	6	1.8	239	2	B72573	hypothetical prote
337	6	1.8	240	2	H69932	hypothetical prote
338	6	1.8	240	2	S77884	hypothetical prote
339	6	1.8	241	2	S75347	hypothetical prote
340	6	1.8	242	1	I40084	gtcR protein - Bac
341	6	1.8	243	2	I50483	vimentin A2 - gold
342	6	1.8	243	2	S37772	ankyrin, erythrocy
343	6	1.8	245	2	B61190	mast cell growth f
344	6	1.8	245	2	A72275	hypothetical prote
345	6	1.8	245	2	G87215	probable secreted
346	6	1.8	247	2	S59523	triose-phosphate i
347	6	1.8	247	2	C83296	hypothetical prote
348	6	1.8	249	2	S59404	hypothetical prote
349	6	1.8	250	2	JC7669	acylglycerol lipas
350	6	1.8	251	2	S25186	probable dehydroge
351	6	1.8	251	2	T06148	hypothetical prote
352	6	1.8	252	1	A34702	amphiregulin precu
353	6	1.8	253	2	H69046	hypothetical prote
354	6	1.8	253	2	B69758	conserved hypothet
355	6	1.8	253	2	A49122	homeobox protein M
356	6	1.8	253	2	JC5347	cdd3 protein - Clo
357	6	1.8	253	2	T52380	zinc finger protei
358	6	1.8	254	1	S39876	gufA protein - Myx
359	6	1.8	254	2	A31488	filaggrin - mouse
360	6	1.8	257	2	C72727	probable ribosomal
361	6	1.8	257	2	S65958	mauJ protein - Par
362	6	1.8	258	1	DHMS	Ig delta chain C r
363	6	1.8	258	1	F69374	conserved hypothet
364	6	1.8	258	2	S10323	type II site-speci
365	6	1.8	258	2	T17895	adenosinetriphosph
366	6	1.8	260	2	I51544	MHC class II beta-
367	6	1.8	260	2	I51542	MHC class II beta-
368	6	1.8	260	2	S71507	restriction endonu
369	6	1.8	260	2	T48846	creatininase (EC 3
370	6	1.8	261	2	AF1679	hypothetical prote
371	6	1.8	261	2	T30170	hypothetical prote
372	6	1.8	262	2	AE1071	ferric iron reduct
373	6	1.8	262	2	T27381	hypothetical prote
374	6	1.8	263	2	T39487	hypothetical prote
375	6	1.8	264	2	T30391	hypothetical prote
376	6	1.8	264	2	D70912	probable monooxyge
377	6	1.8	266	2	A81360	probable disulfide
378	6	1.8	266	2	S02510	nifM protein - Kle
379	6	1.8	267	2	JC6326	2-hydroxypenta-2,4
380	6	1.8	268	2	H83508	probable flagellar
381	6	1.8	268	2	AB2498	hypothetical prote
382	6	1.8	269	2	I51539	MHC class II beta-
383	6	1.8	269	2	I51540	MHC class II beta-
384	6	1.8	269	2	G72550	probable gufA prot
385	6	1.8	270	2	I51543	MHC class II beta-
386	6	1.8	270	2	AH0715	probable inner mem
387	6	1.8	270	2	S61620	probable membrane
388	6	1.8	270	2	F95962	probable taurin up
389	6	1.8	271	2	H83622	hypothetical prote
390	6	1.8	272	1	S39680	hydroxyethylthiazo
391	6	1.8	273	2	S05207	vimentin - pig (fr
392	6	1.8	273	2	A71142	probable UDP-N-ace
393	6	1.8	273	2	H81927	hypothetical prote
394	6	1.8	273	2	H81177	conserved hypothet

395	6	1.8	273	2	A35974	mast cell growth f
396	6	1.8	273	2	A84332	hypothetical prote
397	6	1.8	274	1	A41461	fibronectin-bindin
398	6	1.8	274	2	G83214	probable ATP-bindi
399	6	1.8	274	2	AC2299	cobalt transport A
400	6	1.8	275	2	T03113	hypothetical prote
401	6	1.8	275	2	T42747	hypothetical prote
402	6	1.8	276	2	E95948	hypothetical prote
403	6	1.8	278	2	E82965	hypothetical prote
404	6	1.8	281	2	D71545	probable oligopept
405	6	1.8	283	2	AF2569	hypothetical prote
406	6	1.8	284	2	E89697	protein F48F7.2 [i
407	6	1.8	284	2	B84118	stage II sporulati
408	6	1.8	285	2	T29832	hypothetical prote
409	6	1.8	286	2	E86844	shikimate 5-dehydr
410	6	1.8	286	2	G86950	probable ABC-trans
411	6	1.8	287	2	G81699	peptide ABC transp
412	6	1.8	288	2	S69661	hypothetical prote
413	6	1.8	288	2	F64448	methylviologen-red
414	6	1.8	288	2	AI3400	serine hydroxymeth
415	6	1.8	290	1	WMBEAK	38K phosphoprotein
416	6	1.8	290	1	WMBE1M	38K phosphoprotein
417	6	1.8	290	2	JN0576	carbonate dehydrat
418	6	1.8	290	2	S45349	L1 metallo-beta-la
419	6	1.8	291	1	DHMSM	Ig delta chain C r
420	6	1.8	291	2	AF1722	post-translocation
421	6	1.8	292	2	D64118	cytidine deaminase
422	6	1.8	292	2	F81430	homoserine kinase
423	6	1.8	293	2	S77419	hypothetical prote
424	6	1.8	293	2	T39396	hypothetical prote
425	6	1.8	293	2	AC1352	post-translocation
426	6	1.8	294	1	KFMS3	tissue factor prec
427	6	1.8	294	2	S51008	protein kinase (EC
428	6	1.8	295	2	AD3577	sugar transport sy
429	6	1.8	295	2	S23585	carboxyphosphonoen
430	6	1.8	297	1	S41533	UTP--glucose-1-pho
431	6	1.8	297	1	WJMS29	homeotic protein H
432	6	1.8	297	2	AC0615	conserved hypothet
433	6	1.8	297	2	JC5699	Down syndrome crit
434	6	1.8	298	1	DMHY	desmin - golden ha
435	6	1.8	298	2	T22390	hypothetical prote
436	6	1.8	298	2	S69241	Dreg-5 protein - f
437	6	1.8	298	2	E90550	conserved hypothet
438	6	1.8	298	2	JC5698	Down syndrome crit
439	6	1.8	299	2	T08460	hypothetical prote
440	6	1.8	299	2	AH0245	probable 4-diphosp
441	6	1.8	299	2	A69229	hypothetical prote
442	6	1.8	299	2	A57652	cyclic nucleotide-
443	6	1.8	299	2	A83841	integrase/recombin
444	6	1.8	300	2	B56118	vetispiradiene syn
445	6	1.8	300	2	AH1357	hypothetical prote
446	6	1.8	300	2	AH1727	hypothetical prote
447	6	1.8	301	2	C72359	conserved hypothet
448	6	1.8	301	2	H75470	histone deacetylas
449	6	1.8	301	2	A70731	probable glycerolp
450	6	1.8	301	2	D83970	UDP-N-acetylenolpy
451	6	1.8	302	2	T04109	protein kinase cdc
452	6	1.8	302	2	F81016	conserved hypothet
453	6	1.8	303	2	S12867	carbonate dehydrat
454	6	1.8	303	2	A28620	magainin precursor
455	6	1.8	303	2	E98226	nicotinate-mononuc
456	6	1.8	303	2	E83131	probable transcrip
457	6	1.8	303	2	C70808	hypothetical prote
458	6	1.8	303	2	T25778	hypothetical prote
459	6	1.8	303	2	A49072	bottleneck - fruit
460	6	1.8	304	2	S02284	potassium channel
461	6	1.8	305	2	F72456	hydroxymethylbilan
462	6	1.8	305	2	T41040	conserved hypothet
463	6	1.8	307	2	D86838	hypothetical prote
464	6	1.8	307	2	G69501	UDP-glucose 4-epim
465	6	1.8	307	2	S75469	menaquinone biosyn
466	6	1.8	307	2	A27389	catechol 2,3-dioxy
467	6	1.8	307	2	A42733	catechol 2,3-dioxy
468	6	1.8	307	2	JQ0182	catechol 2,3-dioxy
469	6	1.8	307	2	S47421	catechol 2,3-dioxy
470	6	1.8	307	2	S42100	catechol 2,3-dioxy
471	6	1.8	307	2	T48166	hypothetical prote
472	6	1.8	307	2	G97378	hypothetical prote
473	6	1.8	307	2	AE2596	tonB protein [impo
474	6	1.8	308	2	JC4137	catechol 2,3-dioxy
475	6	1.8	308	2	H96827	protein F20B17.12
476	6	1.8	309	1	DNECTS	terminator sequenc
477	6	1.8	309	2	D90918	hypothetical prote
478	6	1.8	309	2	A85767	hypothetical prote
479	6	1.8	309	2	AH0690	DNA replication te
480	6	1.8	309	2	AF0451	maltose operon per
481	6	1.8	309	2	E96566	F6D8.20 [imported]
482	6	1.8	310	2	E90231	UDP-glucose 4-epim
483	6	1.8	310	2	AC0854	probable LysR-fami
484	6	1.8	310	2	D70745	hypothetical prote
485	6	1.8	311	2	AB1880	hypothetical prote
486	6	1.8	312	2	T33344	hypothetical prote
487	6	1.8	312	2	AB2063	hypothetical prote
488	6	1.8	313	2	H97585	carbohydrate kinas
489	6	1.8	313	2	AI2806	carbohydrate kinas
490	6	1.8	314	2	S35314	transcription fact
491	6	1.8	315	2	S11081	Na+/K+-exchanging
492	6	1.8	315	2	S76267	hypothetical prote
493	6	1.8	315	2	AD3547	ribose transport s
494	6	1.8	316	2	T09591	probable cdc2-like
495	6	1.8	319	2	H69220	photoreactivation-
496	6	1.8	320	1	A39724	homeotic protein H
497	6	1.8	320	2	S41858	hypothetical prote
498	6	1.8	320	2	F75348	hypothetical prote
499	6	1.8	320	2	E71139	hypothetical prote
500	6	1.8	320	2	S18324	lamin C - mouse (f
501	6	1.8	321	2	G86830	thioredoxin reduct
502	6	1.8	321	2	F82104	outer membrane pro
503	6	1.8	321	2	B72604	hypothetical prote
504	6	1.8	321	2	F81030	ABC transporter, p
505	6	1.8	321	2	F81976	probable ferric en
506	6	1.8	322	2	S23053	sloppy paired prot
507	6	1.8	323	1	QXXL1M	NADH dehydrogenase
508	6	1.8	324	2	A69648	2-keto-3-deoxygluc
509	6	1.8	325	2	AF1947	hypothetical prote
510	6	1.8	325	2	S37788	PIR3 protein - yea
511	6	1.8	325	2	T41921	hypothetical prote
512	6	1.8	326	2	S67249	probable membrane
513	6	1.8	327	2	I60169	gonadotropin-relea
514	6	1.8	327	2	E64188	dipeptide transpor
515	6	1.8	327	2	D75196	hypothetical prote
516	6	1.8	327	2	S30405	hypothetical prote
517	6	1.8	328	2	A82180	chemotaxis protein
518	6	1.8	328	2	JC4800	P2Y6 receptor - hu
519	6	1.8	328	2	D83197	probable hydrolase
520	6	1.8	328	2	D81961	conserved hypothet
521	6	1.8	328	2	E64020	hypothetical prote
522	6	1.8	329	1	F69905	probable alcohol d
523	6	1.8	329	2	T37891	delta-aminolevulin
524	6	1.8	330	2	B95394	hypothetical prote
525	6	1.8	330	2	AH0938	cell division prot
526	6	1.8	330	2	B97368	hypothetical sugar
527	6	1.8	330	2	AB2586	pfkB family carboh
528	6	1.8	331	2	T32322	hypothetical prote
529	6	1.8	331	2	AI1879	hypothetical prote
530	6	1.8	333	2	T21595	hypothetical prote
531	6	1.8	333	2	AG3254	glucose-fructose o
532	6	1.8	334	2	S47762	dipeptide transpor
533	6	1.8	334	2	G71228	hypothetical prote
534	6	1.8	334	2	D91181	hypothetical prote
535	6	1.8	334	2	A83662	transcription regu
536	6	1.8	334	2	H86027	hypothetical prote
537	6	1.8	335	2	T31559	hypothetical prote
538	6	1.8	335	2	T31560	hypothetical prote
539	6	1.8	335	2	T31561	hypothetical prote
540	6	1.8	335	2	T41426	hypothetical wtf8

541	6	1.8	335	2	D83142	hypothetical prote
542	6	1.8	335	2	E89819	hypothetical prote
543	6	1.8	336	2	T25180	hypothetical prote
544	6	1.8	336	2	T23902	hypothetical prote
545	6	1.8	336	2	F95925	probable cell-wall
546	6	1.8	337	2	B98333	ribose ABC transpo
547	6	1.8	337	2	AI2949	hypothetical prote
548	6	1.8	337	2	E82727	glucose kinase XF1
549	6	1.8	337	2	AC0668	tellurite resistan
550	6	1.8	337	2	AI0983	dipeptide transpor
551	6	1.8	338	2	C87311	conserved hypothet
552	6	1.8	339	2	T24007	hypothetical prote
553	6	1.8	339	2	JC7712	transcription coac
554	6	1.8	341	2	AI3425	ribose transport s
555	6	1.8	341	2	B82790	conserved hypothet
556	6	1.8	341	2	C89789	hypothetical prote
557	6	1.8	341	2	AG1566	glucitol dehydroge
558	6	1.8	343	2	C84870	probable splicing
559	6	1.8	344	2	A69661	transcription regu
560	6	1.8	344	2	I45774	odorant receptor 1
561	6	1.8	344	2	C97911	hypothetical prote
562	6	1.8	345	2	T24533	hypothetical prote
563	6	1.8	345	2	F98298	pantoate--beta-ala
564	6	1.8	346	2	C83954	MCP-glutamate meth
565	6	1.8	346	2	AH3563	ribose transport s
566	6	1.8	346	2	F75457	conserved hypothet
567	6	1.8	346	2	T44327	hypothetical prote
568	6	1.8	348	2	T37321	Ca2+/calmodulin-de
569	6	1.8	349	2	S67858	gumI protein - Xan
570	6	1.8	352	2	E83519	quinolinate synthe
571	6	1.8	353	2	A95312	probable dioxygena
572	6	1.8	354	2	T36559	probable epoxide h
573	6	1.8	354	2	C83577	hypothetical prote
574	6	1.8	355	2	B87473	acyl-CoA dehydroge
575	6	1.8	355	2	S17704	anthranilate phosp
576	6	1.8	355	2	B40730	class I histocompa
577	6	1.8	355	2	S50372	hypothetical prote
578	6	1.8	356	2	C95134	integrase/recombin
579	6	1.8	356	2	F98002	integrase/recombin
580	6	1.8	357	2	A86825	hypothetical prote
581	6	1.8	357	2	H65041	hypothetical prote
582	6	1.8	357	2	D86707	ABC transporter pe
583	6	1.8	357	2	T24137	hypothetical prote
584	6	1.8	359	2	C97524	hypothetical prote
585	6	1.8	359	2	AD2743	conserved hypothet
586	6	1.8	360	2	C87845	protein T22C1.11 [
587	6	1.8	362	1	LPECRA	rare lipoprotein A
588	6	1.8	362	2	G90712	a minor lipoprotei
589	6	1.8	362	2	C85563	a minor lipoprotei
590	6	1.8	362	2	AC3192	hypothetical prote
591	6	1.8	363	2	B75132	cell division cont
592	6	1.8	363	2	C71073	hypothetical prote
593	6	1.8	363	2	T47588	hypothetical prote
594	6	1.8	364	2	AE2184	extracellular solu
595	6	1.8	365	2	B75398	hypothetical prote
596	6	1.8	366	2	D96649	hypothetical prote
597	6	1.8	366	2	T36035	ion transport prot
598	6	1.8	367	2	S49009	fork head protein
599	6	1.8	367	2	T47517	nuclear receptor b
600	6	1.8	369	2	H88535	protein B0523.4 [i
601	6	1.8	370	2	A60089	transforming prote
602	6	1.8	370	2	S49008	fork head protein
603	6	1.8	370	2	AI2355	hypothetical prote
604	6	1.8	372	1	C70658	probable pepQ - My
605	6	1.8	373	2	G64300	2-hydroxyglutaryl-
606	6	1.8	373	2	B95871	probable CDP-tyvel
607	6	1.8	374	2	D81715	conserved hypothet
608	6	1.8	376	2	A86974	probable cytoplasm
609	6	1.8	377	1	B0AG58	virB10 protein - A
610	6	1.8	377	2	A82713	triacylglycerol li
611	6	1.8	377	2	AF3249	component of type
612	6	1.8	378	2	B27718	cytochrome P450 2C
613	6	1.8	378	2	H70548	hypothetical prote
614	6	1.8	378	2	AH0420	PhnM protein [impo
615	6	1.8	379	2	B55522	lipoprotein D prec
616	6	1.8	379	2	D91078	probable lipoprote
617	6	1.8	379	2	E85923	lipoprotein [impor
618	6	1.8	380	2	T11803	ubiquinol--cytochr
619	6	1.8	380	2	E84644	hypothetical prote
620	6	1.8	380	2	A82244	response regulator
621	6	1.8	381	2	T22334	hypothetical prote
622	6	1.8	381	2	E64050	N-acetylglucosamin
623	6	1.8	381	2	T08722	hypothetical prote
624	6	1.8	383	2	H71848	probable na+/h+ an
625	6	1.8	383	2	G64667	NA+/H+ antiporter
626	6	1.8	384	2	D87471	ROK family protein
627	6	1.8	385	1	S01511	ubiquinol--cytochr
628	6	1.8	385	2	G89956	hypothetical prote
629	6	1.8	385	2	E96797	hypothetical prote
630	6	1.8	386	2	S52981	lycopene cyclase -
631	6	1.8	386	2	C87549	hypothetical prote
632	6	1.8	387	2	E83679	multidrug-efflux t
633	6	1.8	388	2	A82045	cystathionine gamm
634	6	1.8	388	2	S45013	MPT1 protein - yea
635	6	1.8	389	2	D83139	hypothetical prote
636	6	1.8	390	2	AG3180	agrobacterium viru
637	6	1.8	390	2	A83433	translocator prote
638	6	1.8	390	2	T48524	lysophospholipase-
639	6	1.8	391	2	T35470	probable integral
640	6	1.8	392	2	B86847	cation transporter
641	6	1.8	393	2	D95894	probable hydrolase
642	6	1.8	394	2	AH0490	sugar transport sy
643	6	1.8	395	2	C71219	hypothetical prote
644	6	1.8	395	2	JQ0430	hypothetical 44.4K
645	6	1.8	397	2	B86663	multidrug-efflux t
646	6	1.8	399	1	F70427	dihydropteroate sy
647	6	1.8	399	2	AI0322	glycine betaine/L-
648	6	1.8	399	2	G86872	galactokinase (EC
649	6	1.8	399	2	T18566	hypothetical prote
650	6	1.8	399	2	C83847	cytochrome c bioge
651	6	1.8	399	2	F83796	multidrug-efflux t
652	6	1.8	400	2	S30382	glycine hydroxymet
653	6	1.8	400	2	D75331	hypothetical prote
654	6	1.8	401	1	WZBEB1	gene 17 protein -
655	6	1.8	401	2	H83911	hypothetical prote
656	6	1.8	402	2	JE0282	cell division prot
657	6	1.8	403	2	E70618	probable fadE2 pro
658	6	1.8	403	2	F75331	ATP-dependent Clp
659	6	1.8	403	2	C97993	hypothetical prote
660	6	1.8	406	2	D64647	conserved hypothet
661	6	1.8	406	2	AC2267	hypothetical prote
662	6	1.8	407	2	T41708	gtp binding protei
663	6	1.8	407	2	JE0113	zinc-finger protei
664	6	1.8	407	2	S62492	hypothetical PWWP
665	6	1.8	408	2	T44859	glycosyltransferas
666	6	1.8	408	2	D71147	hypothetical prote
667	6	1.8	408	2	F97304	selenocysteine lya
668	6	1.8	408	2	T39570	probable metal tra
669	6	1.8	409	1	B0AG55	virB10 protein - A
670	6	1.8	409	2	T30586	glycosyltransferas
671	6	1.8	409	2	G71936	hypothetical prote
672	6	1.8	409	2	T24138	hypothetical prote
673	6	1.8	410	2	AG2693	large terminase [i
674	6	1.8	412	2	C96816	hypothetical prote
675	6	1.8	412	2	AF3289	transporter, mfs s
676	6	1.8	413	2	E84120	serine hydroxymeth
677	6	1.8	413	2	C90554	hypothetical prote
678	6	1.8	413	2	AC1392	glycine hydroxymet
679	6	1.8	413	2	AE1767	glycine hydroxymet
680	6	1.8	413	2	G85854	probable transport
681	6	1.8	413	2	E82782	phage-related inte
682	6	1.8	414	1	JQ1016	glycine hydroxymet
683	6	1.8	414	2	S75052	hypothetical prote
684	6	1.8	415	1	I40483	glycine hydroxymet
685	6	1.8	415	2	S40911	septin CDC11 - yea
686	6	1.8	415	2	H81079	lipoprotein NlpD,

687	6	1.8	415	2	G81864	probable membrane
688	6	1.8	416	2	F90076	hypothetical prote
689	6	1.8	416	2	G64542	glycine hydroxymet
690	6	1.8	416	2	T50429	dna polymerase gam
691	6	1.8	416	2	A84975	UDP-N-acetylglucos
692	6	1.8	416	2	H64984	hypothetical 43.4
693	6	1.8	416	2	E91010	probable transport
694	6	1.8	418	2	H86848	hypothetical prote
695	6	1.8	419	2	D97475	probable large ter
696	6	1.8	419	2	C95091	conserved hypothet
697	6	1.8	419	2	G97958	conserved hypothet
698	6	1.8	420	1	S34379	glycine hydroxymet
699	6	1.8	421	1	D64100	glycine hydroxymet
700	6	1.8	421	2	S26246	glutamate/aspartat
701	6	1.8	421	2	S26247	glutamate/aspartat
702	6	1.8	421	2	H69490	formylmethanofuran
703	6	1.8	421	2	E86184	hypothetical prote
704	6	1.8	422	2	C98200	serine hydroxymeth
705	6	1.8	422	2	AF3086	serine hydroxymeth
706	6	1.8	422	2	T36626	probable regulator
707	6	1.8	423	2	A64844	ycdB protein precu
708	6	1.8	423	2	A99787	hypothetical prote
709	6	1.8	423	2	A85647	hypothetical prote
710	6	1.8	425	1	H69784	chloramphenicol re
711	6	1.8	425	2	T18592	hypothetical prote
712	6	1.8	425	2	T41172	hypothetical prote
713	6	1.8	425	2	A87631	FMN oxidoreductase
714	6	1.8	426	2	C70896	glycine hydroxymet
715	6	1.8	426	2	D87153	serine hydroxymeth
716	6	1.8	426	2	G83983	C4-dicarboxylate t
717	6	1.8	426	2	H65102	probable tagatose
718	6	1.8	426	2	B91130	probable tagatose
719	6	1.8	426	2	B85975	probable tagatose
720	6	1.8	426	2	AE0907	cytosine deaminase
721	6	1.8	427	2	S75210	glycine hydroxymet
722	6	1.8	427	2	F72341	glycine hydroxymet
723	6	1.8	427	2	AF2406	serine hydroxymeth
724	6	1.8	427	2	A71612	translation releas
725	6	1.8	427	2	F64084	3-deoxy-manno-octu
726	6	1.8	427	2	F90677	cytosine deaminase
727	6	1.8	427	2	E87669	conserved hypothet
728	6	1.8	427	2	E72377	conserved hypothet
729	6	1.8	427	2	S22662	cytosine deaminase
730	6	1.8	427	2	B85528	cytosine deaminase
731	6	1.8	427	2	AC1394	human N-acetylgluc
732	6	1.8	427	2	AF1769	weakly human N-ace
733	6	1.8	428	2	D70343	glycine hydroxymet
734	6	1.8	429	2	AD2720	serine hydroxymeth
735	6	1.8	430	2	AH3420	phage DNA packagin
736	6	1.8	430	2	T26405	hypothetical prote
737	6	1.8	433	2	S76485	hypothetical prote
738	6	1.8	433	2	T01574	indeterminate spik
739	6	1.8	434	2	S30334	glycine hydroxymet
740	6	1.8	434	2	AE0226	conserved hypothet
741	6	1.8	435	2	D82955	probable MFS dicar
742	6	1.8	436	2	F75567	serine hydroxymeth
743	6	1.8	436	2	A81443	probable transmemb
744	6	1.8	436	2	AG0020	cytosine deaminase
745	6	1.8	437	2	JC4288	preprotein translo
746	6	1.8	437	2	S50006	preprotein translo
747	6	1.8	437	2	JC5115	preprotein translo
748	6	1.8	438	2	E55578	hypothetical prote
749	6	1.8	439	2	B70629	hypothetical prote
750	6	1.8	439	2	B44315	cartilage oligomer
751	6	1.8	440	2	A42136	transcription fact
752	6	1.8	440	2	S49765	TyA protein - yeas
753	6	1.8	440	2	F69791	conserved hypothet
754	6	1.8	440	2	S58302	hypothetical prote
755	6	1.8	441	2	T32021	hypothetical prote
756	6	1.8	441	2	C85761	anthranilate synth
757	6	1.8	442	2	D84224	heme synthase [imp
758	6	1.8	443	2	T35974	probable aminoacyl
759	6	1.8	443	2	T37666	26S proteasome reg
760	6	1.8	444	2	T25111	hypothetical prote
761	6	1.8	444	2	E90192	DNA repair protein
762	6	1.8	445	1	A45111	D-alanine/glycine
763	6	1.8	445	2	T21744	hypothetical prote
764	6	1.8	446	2	S75708	hypothetical prote
765	6	1.8	446	2	B70972	hypothetical prote
766	6	1.8	446	2	T39874	hypothetical prote
767	6	1.8	447	2	T12978	hypothetical prote
768	6	1.8	447	2	G95068	cysteinyl-tRNA syn
769	6	1.8	447	2	G97936	cysteine--tRNA lig
770	6	1.8	447	2	T05070	hypothetical prote
771	6	1.8	447	2	A39321	mucin - rat (fragm
772	6	1.8	448	2	I48128	vimentin - Chinese
773	6	1.8	448	2	S57909	probable histidine
774	6	1.8	449	2	S76839	hypothetical prote
775	6	1.8	450	2	AI2324	hypothetical prote
776	6	1.8	450	2	B70506	hypothetical prote
777	6	1.8	451	2	D72422	hypothetical prote
778	6	1.8	451	2	A81206	sugar transporter,
779	6	1.8	451	2	E81781	probable integral
780	6	1.8	453	2	JH0696	plasticin - goldfi
781	6	1.8	453	2	E69755	hypothetical prote
782	6	1.8	453	2	S39866	outer membrane pro
783	6	1.8	454	2	AD2460	hypothetical prote
784	6	1.8	455	1	OOOCG	rhodopsin - giant
785	6	1.8	455	2	A43950	vimentin - common
786	6	1.8	456	2	A60090	peripherin - Afric
787	6	1.8	456	2	F88493	protein F57B9.9 [i
788	6	1.8	457	2	I64229	dihydrolipoamide d
789	6	1.8	457	2	S18239	glycerol-3-phospha
790	6	1.8	457	2	AB1426	GTPase homolog lmo
791	6	1.8	457	2	AH1799	GTPase homolog lin
792	6	1.8	458	2	A43554	desmin - African c
793	6	1.8	458	2	A43549	vimentin 1 - Afric
794	6	1.8	458	2	E82340	probable gluconate
795	6	1.8	458	2	G86561	UDP-N-acetylglucos
796	6	1.8	458	2	D72063	UDP-N-acetylglucos
797	6	1.8	458	2	AD2060	hypothetical prote
798	6	1.8	459	2	H82088	DNA repair protein
799	6	1.8	460	2	A29329	vimentin - chicken
800	6	1.8	460	2	D72694	hypothetical prote
801	6	1.8	460	2	T48137	copper amine oxida
802	6	1.8	461	2	S44733	b0523.4 protein -
803	6	1.8	461	2	T17310	hypothetical prote
804	6	1.8	462	1	S35534	adenovirus E1A enh
805	6	1.8	462	2	I53414	lamin C2 - mouse
806	6	1.8	462	2	AF1694	3-isopropylmalate
807	6	1.8	462	2	T34365	hypothetical prote
808	6	1.8	463	1	DMCH	desmin - chicken
809	6	1.8	463	2	A34285	NADH dehydrogenase
810	6	1.8	463	2	B43549	vimentin 4 - Afric
811	6	1.8	464	1	VEHY	vimentin - golden
812	6	1.8	464	2	A05026	hypothetical prote
813	6	1.8	464	2	T50955	hypothetical prote
814	6	1.8	465	2	F70364	dihydrolipoamide d
815	6	1.8	466	2	A25074	vimentin - human
816	6	1.8	466	2	A43803	vimentin - mouse
817	6	1.8	466	2	S22119	vimentin - rat
818	6	1.8	466	2	T41125	glucose-triggered
819	6	1.8	466	2	T39426	probable ubiquinon
820	6	1.8	469	1	DMHU	desmin - human
821	6	1.8	469	2	I52469	desmin - rat
822	6	1.8	469	2	A24783	desmin - golden ha
823	6	1.8	469	2	A44841	low molecular weig
824	6	1.8	469	2	A54104	desmin - mouse
825	6	1.8	470	2	H72105	dicarboxylase tran
826	6	1.8	470	2	G86516	dicarboxylase tran
827	6	1.8	472	2	S41720	intermediate filam
828	6	1.8	472	2	F90355	multidrug resistan
829	6	1.8	472	2	B99372	multidrug resistan
830	6	1.8	472	2	H70873	probable exported
831	6	1.8	473	2	I54210	N-acetylgalactosam
832	6	1.8	473	2	A48949	beta-glucosidase,

833	6	1.8	473	2	C86841	hypothetical prote
834	6	1.8	474	2	AC1904	hypothetical prote
835	6	1.8	475	1	VHVNSY	nucleoprotein - So
836	6	1.8	476	2	T29083	3-isopropylmalate
837	6	1.8	476	2	AE0916	probable membrane
838	6	1.8	479	2	G82114	sigma-54 dependent
839	6	1.8	479	2	D30411	synapsin IIb - rat
840	6	1.8	479	2	C90457	cytochrome b558/56
841	6	1.8	480	2	G64360	phenylalanine--tRN
842	6	1.8	480	2	T34102	hypothetical prote
843	6	1.8	482	1	BWYMSY	preprotein translo
844	6	1.8	482	2	T44628	probable transposa
845	6	1.8	483	2	AF2363	hypothetical prote
846	6	1.8	484	2	AG2097	serine/threonine k
847	6	1.8	485	2	I39699	3-isopropylmalate
848	6	1.8	486	2	A98308	attK protein (U594
849	6	1.8	486	2	AB2975	succinate semialde
850	6	1.8	486	2	B70539	hypothetical prote
851	6	1.8	487	1	O4RBC6	cytochrome P450 2C
852	6	1.8	487	1	O4RBP4	progesterone monoo
853	6	1.8	487	1	S71770	calcium-dependent
854	6	1.8	487	2	A26731	cytochrome P450 2C
855	6	1.8	487	2	B91122	hypothetical prote
856	6	1.8	487	2	A85967	hypothetical prote
857	6	1.8	487	2	A64642	conserved hypothet
858	6	1.8	487	2	B71873	hypothetical prote
859	6	1.8	489	2	C65147	hypothetical 53.7
860	6	1.8	489	2	H91174	probable transport
861	6	1.8	489	2	H86020	probable transport
862	6	1.8	489	2	D98312	hypothetical prote
863	6	1.8	489	2	AF2970	conserved hypothet
864	6	1.8	490	1	G69282	hypothetical prote
865	6	1.8	490	2	A25954	cytochrome P450 2C
866	6	1.8	490	2	A32140	steroid 15beta-mon
867	6	1.8	490	2	I48162	cytochrome P450 -
868	6	1.8	490	2	I48163	cytochrome P450 -
869	6	1.8	490	2	I48189	cytochrome P450 II
870	6	1.8	490	2	I49610	cytochrome P450 -
871	6	1.8	490	2	I52410	cytochrome P450 II
872	6	1.8	490	2	A36122	cytochrome P450 2C
873	6	1.8	490	2	H95033	xanthine/uracil pe
874	6	1.8	490	2	H97904	conserved hypothet
875	6	1.8	490	2	A55141	GlcNAc beta-1,4-N-
876	6	1.8	490	2	AB2335	hypothetical prote
877	6	1.8	491	2	H97501	serine hydroxymeth
878	6	1.8	491	2	S44657	cosmid ZK353 prote
879	6	1.8	491	2	F70699	probable pbpA prot
880	6	1.8	492	2	S75049	hypothetical prote
881	6	1.8	494	2	A89930	glucose-6-phosphat
882	6	1.8	494	2	I52658	neurofilament-66 -
883	6	1.8	495	2	F86469	protein F12K21.8 [
884	6	1.8	496	2	S68160	probable RNA bindi
885	6	1.8	498	2	T04640	hypothetical prote
886	6	1.8	499	2	F84149	transposase (25) B
887	6	1.8	500	2	T39186	glucose-6-phosphat
888	6	1.8	501	2	B71707	ADP,ATP carrier pr
889	6	1.8	501	2	B97790	aDP,ATP carrier pr
890	6	1.8	501	2	D87613	pilus assembly pro
891	6	1.8	501	2	T48595	protoporphyrinogen
892	6	1.8	502	2	S10505	nicotinic acetylch
893	6	1.8	503	2	C69277	2-isopropylmalate
894	6	1.8	503	2	AC0062	conserved hypothet
895	6	1.8	504	2	I53868	alpha-internexin -
896	6	1.8	505	2	C82216	probable fumarate
897	6	1.8	505	2	A41023	alpha-internexin -
898	6	1.8	506	2	B84339	hypothetical prote
899	6	1.8	506	2	E70200	hypothetical prote
900	6	1.8	506	2	T35261	probable metallope
901	6	1.8	507	2	A83105	probable fumarase
902	6	1.8	508	1	JC5713	25-hydroxyvitamin
903	6	1.8	508	2	C87564	cell division prot
904	6	1.8	508	2	T37224	hypothetical prote
905	6	1.8	509	1	TVHAST	protein-tyrosine k
906	6	1.8	509	2	T07721	hypothetical prote
907	6	1.8	509	2	AC2217	hypothetical prote
908	6	1.8	510	2	F75115	co-induced hydroge
909	6	1.8	510	2	A87482	conserved hypothet
910	6	1.8	510	2	AI2689	two component sens
911	6	1.8	511	2	A54676	antiquitin - human
912	6	1.8	511	2	D70944	probable lipT prot
913	6	1.8	513	2	D69016	serine--tRNA ligas
914	6	1.8	513	2	AB2504	hypothetical prote
915	6	1.8	513	2	D98225	hypothetical prote
916	6	1.8	513	2	AC3061	hypothetical prote
917	6	1.8	514	2	T15944	hypothetical prote
918	6	1.8	515	2	T30651	hypothetical prote
919	6	1.8	515	2	B96825	hypothetical prote
920	6	1.8	515	2	D97471	hypothetical senso
921	6	1.8	516	2	A84081	hypothetical prote
922	6	1.8	517	2	T44289	probable methylmal
923	6	1.8	518	2	T11289	cytochrome-c oxida
924	6	1.8	520	1	NNEC1	anthranilate synth
925	6	1.8	520	2	D90858	anthranilate synth
926	6	1.8	520	2	A83203	alginate o-acetylt
927	6	1.8	521	2	A86909	hypothetical prote
928	6	1.8	523	2	S39899	rnfF protein precu
929	6	1.8	523	2	C95303	conserved hypothet
930	6	1.8	524	1	S76810	probable NADH dehy
931	6	1.8	524	2	E81678	glucose-6-phosphat
932	6	1.8	524	2	A75588	probable protein k
933	6	1.8	525	2	F71521	probable glucose-6
934	6	1.8	526	2	F86618	glucose-6-P isomer
935	6	1.8	526	2	C72005	glucose-6-p isomer
936	6	1.8	526	2	B81533	glucose-6-phosphat
937	6	1.8	526	2	S03600	cell surface antig
938	6	1.8	526	2	T08541	hypothetical prote
939	6	1.8	527	2	S64702	cell surface antig
940	6	1.8	527	2	A75399	hypothetical prote
941	6	1.8	529	2	T18589	chaperonin beta ch
942	6	1.8	529	2	E84813	hypothetical prote
943	6	1.8	530	2	C82344	phosphoribosylamin
944	6	1.8	530	2	T06237	probable high affi
945	6	1.8	530	2	A84922	hypothetical prote
946	6	1.8	531	2	A84444	hypothetical prote
947	6	1.8	532	1	QFPGM	neurofilament trip
948	6	1.8	532	2	H83993	two-component sens
949	6	1.8	532	2	G87912	protein B0205.9 [i
950	6	1.8	535	2	D84340	hypothetical prote
951	6	1.8	536	2	AI3544	aldehyde dehydroge
952	6	1.8	537	2	F97546	hypothetical prote
953	6	1.8	537	2	AB2766	sulfate permease [
954	6	1.8	538	2	T28874	hypothetical prote
955	6	1.8	540	2	G83589	probable phosphate
956	6	1.8	541	2	T34850	probable acid--CoA
957	6	1.8	541	2	C70789	probable peptidetr
958	6	1.8	544	2	G69072	conserved hypothet
959	6	1.8	544	2	T17547	proline-rich prote
960	6	1.8	544	2	AE3375	methionyl-tRNA syn
961	6	1.8	545	2	B44054	orf2 protein - Jun
962	6	1.8	546	2	B97645	integral membrane
963	6	1.8	551	2	G95099	DNA polymerase III
964	6	1.8	551	2	A97968	DNA-directed DNA p
965	6	1.8	552	2	F69817	conserved hypothet
966	6	1.8	553	2	C75318	hypothetical prote
967	6	1.8	555	1	S24061	transcription fact
968	6	1.8	555	2	I53869	zinc finger protei
969	6	1.8	555	2	T45351	ferredoxin [import
970	6	1.8	557	2	AE0204	methyl-accepting c
971	6	1.8	558	2	B99494	dihydroxy-acid deh
972	6	1.8	558	2	F64235	Na+ ATPase chain J
973	6	1.8	560	2	T19622	hypothetical prote
974	6	1.8	560	2	D84205	hypothetical prote
975	6	1.8	561	2	AG1861	hypothetical prote
976	6	1.8	562	2	T32581	hypothetical prote
977	6	1.8	563	2	E70752	probable deaD prot
978	6	1.8	564	2	T12550	hypothetical prote

979	6	1.8	565	2	B70652	probable cysG prot
980	6	1.8	565	2	S73707	Na(+) translocatin
981	6	1.8	567	2	F87594	conserved hypothet
982	6	1.8	568	2	A89958	acetyl-CoA synthet
983	6	1.8	569	2	S64957	aspergillopepsin I
984	6	1.8	569	2	T01399	hypothetical prote
985	6	1.8	570	2	G72595	hypothetical prote
986	6	1.8	571	1	S30253	GABA transport pro
987	6	1.8	572	1	VEHULC	lamin C - human
988	6	1.8	572	2	S77249	hypothetical prote
989	6	1.8	572	2	T29880	hypothetical prote
990	6	1.8	573	2	AI3332	urease alpha chain
991	6	1.8	574	2	S04333	lamin C - mouse
992	6	1.8	574	2	C82301	endoglucanase-rela
993	6	1.8	574	2	T51799	CLB1-like protein
994	6	1.8	576	2	AB0863	L-fuculose isomera
995	6	1.8	577	1	DNBYPA	polyadenylate-bind
996	6	1.8	579	2	AF1788	DNA polymerase III
997	6	1.8	579	2	AG1412	DNA polymerase III
998	6	1.8	580	2	T30583	probable peptide s
999	6	1.8	581	2	T36267	probable glutamyl-
1000	6	1.8	581	2	T05550	hypothetical prote

ALIGNMENTS

RESULT 1
C65015
hypothetical protein b2412 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: C65015
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: C65015
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-328 <BLAT>
A;Cross-references: GB:AE000329; GB:U00096; NID:g2367137; PIDN:AAC75465.1; PID:g1788752;
A;Experimental source: strain K-12, substrain MG1655

Query Match 69.2%; Score 227; DB 2; Length 328;
Best Local Similarity 99.7%; Pred. No. 6.9e-225;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60

Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAPH 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAPH 120

Qy     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180

Qy     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGEALLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240
           ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGELLLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240

Qy     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300

Qy     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328
           ||||||||||||||||||||||||||||
Db     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328
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RESULT 2
D91039
cell division protein involved in FtsZ ring [imported] - Escherichia coli (strain O15
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D91039
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91039
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36707.1; PID:g13362754; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3284

Query Match 36.3%; Score 119; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 5.9e-114;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60

Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAP 119
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAP 119
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RESULT 3
G85883
cell division protein involved in FtsZ ring [imported] - Escherichia coli (strain O15
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85883
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85883
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <STO>
A;Cross-references: GB:AE005174; NID:g12516785; PIDN:AAG57531.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: zipA

Query Match 35.7%; Score 117; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.6e-112;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60

Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQH 117
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQH 117
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RESULT 4
AB0810
cell division protein [imported] - Salmonella enterica subsp. enterica serovar Typhi

```
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0810
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AB0810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07660.1; PID:g16503647; GSPDB:GN00176
C;Genetics:
A;Gene: STY2664

  Query Match             16.5%;  Score 54;  DB 2;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-47;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYD 54
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYD 54


RESULT   5
AG0363
probable cell division protein YPO2990 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AG0363
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0363
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92234.1; PID:g15980946; GSPDB:GN00175
C;Genetics:
A;Gene: YPO2990

  Query Match              3.4%;  Score 11;  DB 2;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 0.005;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     242 LFSLANMVKPG 252
           ||||||||||| 
Db     239 LFSLANMVKPG 249


RESULT   6
T22308
hypothetical protein F46F2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22308
R;Thomas, K.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19545
A;Accession: T22308
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-137 <WIL>
A;Cross-references: EMBL:Z69903; PIDN:CAA93772.1; GSPDB:GN00028; CESP:F46F2.3
A;Experimental source: clone F46F2
C;Genetics:
A;Gene: CESP:F46F2.3
A;Map position: X
A;Introns: 76/3

  Query Match              2.7%;  Score 9;  DB 2;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     126 QQPAYQPQP 134
           |||||||||
Db      67 QQPAYQPQP 75


RESULT   7
D84353
hypothetical protein Vng2029h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84353
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
 Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: D84353
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-130 <STO>
A;Cross-references: GB:AE004437; NID:g10581457; PIDN:AAG20192.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG2029H

  Query Match              2.4%;  Score 8;  DB 2;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     166 PAEPVAAP 173
           ||||||||
Db      74 PAEPVAAP 81


RESULT   8
S37920
MBR1 protein precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL093w; protein YKL440
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C;Accession: S37920; S39093; S37919; S42004; S45577; S27427; S39116
R;Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; P
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37920
A;Accession: S37920
A;Molecule type: DNA
A;Residues: 1-275 <CHR>
A;Cross-references: EMBL:Z28093; MIPS:YKL093w
A;Experimental source: strain S288C
R;Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Sor, F.; Bolotin-Fuku
Yeast 9, 1149-1155, 1993
A;Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically
 protein kinases.
A;Reference number: S39084; MUID:94078677
A;Accession: S39093
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <PAL>
A;Cross-references: EMBL:X71133; NID:g431205; PIDN:CAA50464.1; PID:g450764
A;Experimental source: strain S288C
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R;James, C.M.; Gent, M.E.; Indge, K.J.; Oliver, S.G.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37918
A;Accession: S37919
A;Molecule type: DNA
A;Residues: 169-339 <JAM>
A;Cross-references: EMBL:Z28093; MIPS:YKL093w
A;Experimental source: strain S288C
R;James, C.M.; Gent, M.E.; Oliver, S.G.
Yeast 10, 257-264, 1994
A;Title: Sequence analysis of a 3.5 Kb EcoRI fragment from the left arm of Saccharomyces
rotein.
A;Reference number: S42004; MUID:94262329
A;Accession: S42004
A;Molecule type: DNA
A;Residues: 169-339 <JA2>
A;Cross-references: EMBL:X75561; NID:g414687; PIDN:CAA53240.1; PID:g414688
A;Experimental source: strain S288C
R;Daignan-Fornier, B.; Nguyen, C.C.; Reisdorf, P.; Lemeignan, B.; Bolotin-Fukuhara, M.
Mol. Gen. Genet. 243, 575-583, 1994
A;Title: MBR1 and MBR3, two related yeast genes that can suppress the growth defect of H
A;Reference number: S45577; MUID:94268503
A;Accession: S45577
A;Molecule type: DNA
A;Residues: 1-87,'G',89-167,'R',169-205,'T',207-244,'E',246-339 <DAI>
A;Cross-references: EMBL:M63309; NID:g171907; PID:g171908
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MBR1
A;Cross-references: SGD:S0001576; MIPS:YKL093w
A;Map position: 11L
A;Genome: nuclear
C;Keywords: mitochondrion


  Query Match             2.4%;  Score 8;  DB 2;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     100 QPRQPVQQ 107
           ||||||||
Db     305 QPRQPVQQ 312


RESULT   9
AE0990
probable membrane protein STY4230 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE0990
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0990
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08049.1; PID:g16505029; GSPDB:GN00176
C;Genetics:
A;Gene: STY4230
C;Superfamily: hypothetical protein b2322


  Query Match             2.4%;  Score 8;  DB 2;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEPA 182
           ||||||||
Db       2 PEPVAEPA 9


RESULT  10
S47692
hypothetical 43.8K protein (ftsY-nikA intergenic region) - Escherichia coli
N;Alternate names: hypothetical protein f419
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S47692; D65144
R;Plunkett, G.
submitted to the EMBL Data Library, March 1994
A;Reference number: S47666
A;Accession: S47692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <PLU>
A;Cross-references: EMBL:U00039; NID:g466582; PID:g912459
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D65144
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-419 <BLAT>
A;Cross-references: GB:AE000423; GB:U00096; NID:g1789880; PIDN:AAC76498.1; PID:g17898
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yhhS
A;Start codon: GTG
C;Superfamily: hypothetical protein b2322


  Query Match             2.4%;  Score 8;  DB 1;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEPA 182
           ||||||||
Db      16 PEPVAEPA 23


RESULT  11
B91169
probable transport ECs4322 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: B91169
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37745.1; PID:g13363796; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4322
C;Superfamily: hypothetical protein b2322


  Query Match             2.4%;  Score 8;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEPA 182
           ||||||||
```

```
Db     16 PEPVAEPA 23


RESULT  12
B86015
probable transport yhhS [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B86015
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86015
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <STO>
A;Cross-references: GB:AE005174; NID:g12518132; PIDN:AAG58582.1; GSPDB:GN00145; UWGP:Z48
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yhhS
C;Superfamily: hypothetical protein b2322


  Query Match             2.4%;  Score 8;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEPA 182
           ||||||||
Db      16 PEPVAEPA 23


RESULT  13
G86773
citrate (pro-3S)-lyase (EC 4.1.3.6) alpha chain [imported] - Lactococcus lactis subsp. l
N;Alternate names: citrate lyase alpha chain
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86773
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86773
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: GB:AE005176; PID:g12724158; PIDN:AAK05289.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: citF
C;Superfamily: Escherichia citrate (pro-3S)-lyase alpha chain
C;Keywords: carbon-carbon lyase; oxo-acid-lyase


  Query Match             2.4%;  Score 8;  DB 2;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 8.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     318 DIIREVKD 325
           ||||||||
Db     505 DIIREVKD 512


RESULT  14
B97566
hypothetical protein AGR_C_3142 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: B97566
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
A;Accession: B97566
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-912 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87483.1; PID:g15156806; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_3142
A;Map position: circular chromosome


  Query Match             2.4%;  Score 8;  DB 2;  Length 912;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     146 VAPAPQPV 153
           ||||||||
Db     350 VAPAPQPV 357


RESULT  15
AH2786
conserved hypothetical protein Atu1710 [imported] - Agrobacterium tumefaciens (strain
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH2786
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AH2786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1008 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42710.1; PID:g17740147; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1710
A;Map position: circular chromosome


  Query Match             2.4%;  Score 8;  DB 2;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     146 VAPAPQPV 153
           ||||||||
Db     446 VAPAPQPV 453


Search completed: September 25, 2002, 09:53:30
Job time: 159 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 25, 2002, 09:52:56 ; Search time 13.47 Seconds
(without alignments)
942.837 Million cell updates/sec

Title: US-09-184-826-2
Perfect score: 328
Sequence: 1 MMQDLRLILIIVGAIAIIAL.....TPQKLREYQDIIREVKDANA 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	328	100.0	328	1	ZIPA_ECOLI	P77173 escherichia
2	54	16.5	328	1	ZIPA_SALTY	P55894 salmonella
3	11	3.4	328	1	ZIPA_YERPE	P58492 yersinia pe
4	8	2.4	339	1	MBR1_YEAST	P23493 saccharomyc
5	8	2.4	419	1	YHHS_ECOLI	P37621 escherichia
6	8	2.4	541	1	BCHB_CHLAU	Q9f6x5 chloroflexu
7	8	2.4	591	1	ALU8_HUMAN	P39195 homo sapien
8	8	2.4	593	1	ALU7_HUMAN	P39194 homo sapien
9	7	2.1	49	1	LHA3_ECTHA	P80107 ectothiorho
10	7	2.1	178	1	RL17_LEPIN	Q9xd08 leptospira
11	7	2.1	206	1	RS3A_HALN1	Q9hra5 halobacteri
12	7	2.1	255	1	GRPS_MYXXA	P95333 myxococcus
13	7	2.1	277	1	TRT1_HUMAN	P13805 homo sapien
14	7	2.1	288	1	ALF_MYCGE	P47269 mycoplasma
15	7	2.1	289	1	ZIPA_PSEAE	Q9i3i5 pseudomonas
16	7	2.1	291	1	ZIPA_VIBCH	Q9ktd2 vibrio chol
17	7	2.1	293	1	KHSE_PYRHO	O58814 pyrococcus
18	7	2.1	328	1	HEMB_BACHD	Q9k8g2 bacillus ha
19	7	2.1	330	1	RIL_HUMAN	P50479 homo sapien
20	7	2.1	362	1	CD44_CRIGR	P20944 cricetulus
21	7	2.1	401	1	CASP_HUMAN	O75718 homo sapien
22	7	2.1	431	1	CD44_MESAU	Q60522 m cd44 anti
23	7	2.1	463	1	NU4M_STRPU	P15551 strongyloce
24	7	2.1	466	1	ZIC3_MOUSE	Q62521 mus musculu
25	7	2.1	467	1	ZIC3_HUMAN	O60481 homo sapien
26	7	2.1	482	1	TRPE_SPIAU	P21690 spirochaeta
27	7	2.1	487	1	TTDT_ECOLI	P39414 escherichia
28	7	2.1	500	1	NU4C_OENHO	P58419 oenothera h
29	7	2.1	502	1	YH60_MYCTU	O06795 mycobacteri
30	7	2.1	503	1	CD44_RAT	P26051 rattus norv
31	7	2.1	506	1	UDPG_SCHPO	P78811 schizosacch
32	7	2.1	511	1	KLFB_MOUSE	Q9epf4 mus musculu
33	7	2.1	512	1	KLFB_HUMAN	O14901 homo sapien
34	7	2.1	579	1	SYN3_RAT	O70441 rattus norv
35	7	2.1	583	1	FTSZ_AGRTU	O30992 agrobacteri
36	7	2.1	585	1	ALU5_HUMAN	P39192 homo sapien
37	7	2.1	655	1	CD44_MOUSE	P15379 mus musculu
38	7	2.1	676	1	VGP_EBOIC	Q66810 ebola virus
39	7	2.1	676	1	VGP_EBOSB	Q66814 ebola virus
40	7	2.1	676	1	VGP_EBOSM	Q66798 ebola virus
41	7	2.1	677	1	VGP_EBORE	Q66799 ebola virus
42	7	2.1	677	1	VGP_EBORS	Q89853 ebola virus
43	7	2.1	1006	1	EPB6_HUMAN	O15197 homo sapien
44	7	2.1	1014	1	EPB6_MOUSE	O08644 mus musculu
45	7	2.1	1018	1	HMW1_MYCPN	Q50365 mycoplasma
46	7	2.1	1073	1	YFD4_YEAST	P43564 saccharomyc
47	7	2.1	1242	1	TBP7_CAEEL	P54816 caenorhabdi
48	7	2.1	1362	1	BRD4_HUMAN	O60885 homo sapien
49	7	2.1	1553	1	TP2A_CHICK	O42130 gallus gall
50	7	2.1	1782	1	VIT_BOMMO	Q27309 bombyx mori
51	7	2.1	6359	1	BACC_BACLI	O68008 b bacitraci
52	6	1.8	41	1	PSAJ_CHLVU	P56340 chlorella v
53	6	1.8	42	1	PSAJ_NEPOL	Q9tkz8 nephroselmi
54	6	1.8	79	1	OAG3_SALTY	P58651 salmonella
55	6	1.8	82	1	HFQ_CAUCR	Q9a7h8 caulobacter
56	6	1.8	88	1	RS16_BACST	P81290 bacillus st
57	6	1.8	92	1	RL6_ENTHI	O15595 entamoeba h
58	6	1.8	93	1	YP83_YEAST	O14464 saccharomyc
59	6	1.8	95	1	FER_MARPO	P09735 marchantia
60	6	1.8	98	1	CYTA_BOVIN	P80416 bos taurus
61	6	1.8	98	1	YAM3_YEAST	P39559 saccharomyc
62	6	1.8	110	1	YC27_ARCFU	O29041 archaeoglob
63	6	1.8	111	1	RL22_CHLTR	O84528 chlamydia t
64	6	1.8	121	1	AMEL_ORNAN	O97646 ornithorhyn
65	6	1.8	121	1	FLIO_ECOLI	P22586 escherichia
66	6	1.8	122	1	RL14_SPICI	O31165 spiroplasma
67	6	1.8	124	1	BCGF_HUMAN	P20931 homo sapien
68	6	1.8	126	1	CLP2_DROMI	P91629 drosophila
69	6	1.8	126	1	SYN2_MOUSE	Q64332 mus musculu
70	6	1.8	128	1	C562_ECOLI	P00192 escherichia
71	6	1.8	131	1	PRO5_ARATH	Q9fe63 arabidopsis
72	6	1.8	133	1	REV_CAEVC	P33460 caprine art
73	6	1.8	138	1	CLP1_DROMI	P91627 drosophila
74	6	1.8	139	1	FLAF_METJA	Q58307 methanococc
75	6	1.8	139	1	YO72_RHIME	P42879 rhizobium m
76	6	1.8	141	1	LSHB_CERSI	O77835 ceratotheri
77	6	1.8	142	1	E1BS_ADE04	P10406 human adeno
78	6	1.8	143	1	IF1A_RABIT	P47814 oryctolagus
79	6	1.8	144	1	R12A_ARATH	Q9s9p1 arabidopsis
80	6	1.8	146	1	RL28_TRYCR	O00822 trypanosoma
81	6	1.8	147	1	RS9_AQUAE	O67723 aquifex aeo
82	6	1.8	150	1	ALL5_HEVBR	Q39967 hevea brasi
83	6	1.8	155	1	NU6M_CANPA	P48923 candida par
84	6	1.8	156	1	COAD_HAEIN	P44805 haemophilus
85	6	1.8	157	1	COAD_HELPJ	Q9zje4 helicobacte
86	6	1.8	157	1	COAD_HELPY	O26010 helicobacte
87	6	1.8	158	1	COAD_CAMJE	Q9ppf2 campylobact
88	6	1.8	158	1	COAD_PASMU	Q9cld4 pasteurella
89	6	1.8	159	1	COAD_ECOLI	P23875 escherichia
90	6	1.8	159	1	COAD_KLEPN	Q9xc89 klebsiella
91	6	1.8	159	1	COAD_PSEAE	Q9i6d1 pseudomonas
92	6	1.8	160	1	COTF_BACSU	P23261 bacillus su
93	6	1.8	161	1	COAD_AQUAE	O66614 aquifex aeo
94	6	1.8	161	1	COAD_SERMA	Q9x980 serratia ma
95	6	1.8	161	1	GLB9_CHITH	P02223 chironomus
96	6	1.8	161	1	GLBC_CHITH	P12548 chironomus
97	6	1.8	161	1	GLBD_CHITH	P12292 chironomus
98	6	1.8	161	1	GLBE_CHITH	P11583 chironomus
99	6	1.8	161	1	GLBF_CHITH	P12549 chironomus
100	6	1.8	161	1	GLBI_CHITH	Q23763 chironomus
101	6	1.8	161	1	GLBI_CHITP	P18966 chironomus
102	6	1.8	161	1	GLBK_CHITH	Q23762 chironomus
103	6	1.8	162	1	COAD_XYLFA	Q9pep8 xylella fas
104	6	1.8	162	1	RS16_MYCTU	Q10795 mycobacteri
105	6	1.8	163	1	COAD_CAUCR	P58103 caulobacter
106	6	1.8	163	1	GLBZ_CHITH	Q23761 chironomus

107	6	1.8	163	1	GLBZ_CHITP	P29245	chironomus
108	6	1.8	164	1	COAD_VIBCH	Q9kvc4	vibrio chol
109	6	1.8	165	1	COAD_BUCAI	P57643	buchnera ap
110	6	1.8	165	1	COAD_BUCAP	Q9z613	buchnera ap
111	6	1.8	165	1	SSB_PSEAE	P40947	pseudomonas
112	6	1.8	169	1	COAD_CHRVI	P71154	chromatium
113	6	1.8	172	1	Y21B_METJA	P81232	methanococc
114	6	1.8	176	1	22P2_RAT	P22283	rattus norv
115	6	1.8	178	1	COAD_ZYMMO	Q9rme4	zymomonas m
116	6	1.8	179	1	APT_HELPJ	Q9zlq9	helicobacte
117	6	1.8	179	1	APT_HELPY	O25296	helicobacte
118	6	1.8	180	1	CH19_DROSU	P13428	drosophila
119	6	1.8	181	1	APT_DROPS	P54363	drosophila
120	6	1.8	181	1	OLEO_HELAN	P29529	helianthus
121	6	1.8	184	1	NUSG_BORBU	O51355	borrelia bu
122	6	1.8	185	1	NU6M_SARGL	O63849	sarcophyton
123	6	1.8	185	1	YCXB_BACSU	Q08793	bacillus su
124	6	1.8	187	1	RPOE_LACLA	Q9cht4	lactococcus
125	6	1.8	193	1	BPA2_PSES1	Q52439	pseudomonas
126	6	1.8	193	1	Y274_CHLMU	Q9pl34	chlamydia m
127	6	1.8	195	1	COAE_CORGL	P56187	corynebacte
128	6	1.8	197	1	YKGB_ECOLI	P75685	escherichia
129	6	1.8	202	1	AMEL_MONDO	Q28462	monodelphis
130	6	1.8	202	1	NU6M_METSE	O47498	metridium s
131	6	1.8	204	1	SOMA_ODOAR	Q9i915	odontesthes
132	6	1.8	205	1	NEF_SIVCZ	P17664	chimpanzee
133	6	1.8	209	1	PROQ_HAEIN	P44286	haemophilus
134	6	1.8	211	1	TUB8_SOLTU	P33191	solanum tub
135	6	1.8	213	1	OS24_PLABA	Q04620	plasmodium
136	6	1.8	215	1	RK4_ODOSI	P49546	odontella s
137	6	1.8	219	1	RB3D_HUMAN	O95716	homo sapien
138	6	1.8	220	1	MTHH_HUMAN	O43709	homo sapien
139	6	1.8	222	1	TOXK_PICFA	P19972	p salt-medi
140	6	1.8	228	1	IFE2_CAEEL	Q21693	caenorhabdi
141	6	1.8	230	1	YX09_CAEEL	Q11115	caenorhabdi
142	6	1.8	237	1	FIXK_BRAJA	P29286	bradyrhizob
143	6	1.8	240	1	YPBE_BACSU	P50731	bacillus su
144	6	1.8	243	1	VIM2_CARAU	P48672	carassius a
145	6	1.8	245	1	BZLF_EBV	P03206	epstein-bar
146	6	1.8	250	1	TPIS_GRAVE	P48492	gracilaria
147	6	1.8	251	1	YMP3_STRCO	P43168	streptomyce
148	6	1.8	252	1	AMPR_HUMAN	P15514	homo sapien
149	6	1.8	253	1	MOX1_MOUSE	P32442	mus musculu
150	6	1.8	253	1	RS4E_AERPE	Q9yf85	aeropyrum p
151	6	1.8	254	1	GUFA_MYXXA	Q06916	myxococcus
152	6	1.8	257	1	T2C2_HAEIN	P17743	haemophilus
153	6	1.8	258	1	DTC_MOUSE	P01881	mus musculu
154	6	1.8	263	1	PFLA_STRMU	O68575	streptococc
155	6	1.8	266	1	NIFM_KLEPN	P08534	klebsiella
156	6	1.8	269	1	T2S1_STRFI	O52512	streptomyce
157	6	1.8	272	1	THIM_BACSU	P39593	bacillus su
158	6	1.8	273	1	SCF_HUMAN	P21583	homo sapien
159	6	1.8	274	1	P30_MYCPN	P75330	mycoplasma
160	6	1.8	275	1	VIME_PIG	P02543	sus scrofa
161	6	1.8	285	1	ARSB_MOUSE	P50429	mus musculu
162	6	1.8	286	1	AROE_LACLA	Q9ces7	lactococcus
163	6	1.8	287	1	MAUJ_PARDE	P22566	paracoccus
164	6	1.8	289	1	CAH8_HUMAN	P35219	homo sapien
165	6	1.8	290	1	BLA1_XANMA	P52700	xanthomonas
166	6	1.8	290	1	CAH8_MOUSE	P28651	mus musculu
167	6	1.8	290	1	VP38_HSVMG	P30023	marek's dis
168	6	1.8	291	1	DTCM_MOUSE	P01882	mus musculu
169	6	1.8	292	1	CDD_HAEIN	P44325	haemophilus
170	6	1.8	292	1	KHSE_CAMJE	Q9piz3	campylobact
171	6	1.8	294	1	CDK5_DROME	P48609	drosophila
172	6	1.8	294	1	CPPM_STRHY	P11435	streptomyce
173	6	1.8	294	1	MTA1_SOREQ	O13595	sordaria eq
174	6	1.8	294	1	TF_MOUSE	P20352	mus musculu
175	6	1.8	295	1	TF_RAT	P42533	rattus norv
176	6	1.8	297	1	DSR3_HUMAN	O14972	homo sapien
177	6	1.8	297	1	DSR3_MOUSE	O35075	mus musculu
178	6	1.8	297	1	GALF_SHIFL	P37776	shigella fl
179	6	1.8	297	1	HXB1_MOUSE	P17919	mus musculu
180	6	1.8	298	1	REG5_DROME	Q94913	drosophila
181	6	1.8	298	1	STX2_CAEEL	Q20574	caenorhabdi
182	6	1.8	301	1	MURB_BACHD	Q9k9t1	bacillus ha
183	6	1.8	301	1	YM77_MYCTU	Q50687	mycobacteri
184	6	1.8	302	1	HSLO_NEIMA	Q9jwc8	neisseria m
185	6	1.8	302	1	HSLO_NEIMB	Q9jxk1	neisseria m
186	6	1.8	303	1	BNK_DROME	P40794	drosophila
187	6	1.8	303	1	MAGA_XENLA	P11006	xenopus lae
188	6	1.8	305	1	HEM3_AERPE	Q9y9j0	aeropyrum p
189	6	1.8	307	1	DMPB_PSESP	P17262	pseudomonas
190	6	1.8	307	1	MENA_SYNY3	P73962	synechocyst
191	6	1.8	307	1	NAHH_PSEPU	P08127	pseudomonas
192	6	1.8	307	1	XYE2_PSEPU	Q04285	pseudomonas
193	6	1.8	309	1	TUS_ECO57	P58384	escherichia
194	6	1.8	309	1	TUS_ECOLI	P16525	escherichia
195	6	1.8	309	1	TUS_SALTY	O52714	salmonella
196	6	1.8	310	1	TUS_KLEPO	O52715	klebsiella
197	6	1.8	310	1	Y497_MYCTU	Q11162	mycobacteri
198	6	1.8	313	1	B3GT_DROME	O97422	drosophila
199	6	1.8	314	1	IKBA_PIG	Q08353	sus scrofa
200	6	1.8	315	1	ATNB_ARTSA	P25169	artemia sal
201	6	1.8	315	1	SECF_SYNY3	Q55611	synechocyst
202	6	1.8	319	1	URED_SYNPV	O87399	synechococc
203	6	1.8	320	1	HXA4_HUMAN	Q00056	homo sapien
204	6	1.8	321	1	AOC3_RAT	O08590	rattus norv
205	6	1.8	322	1	SLP1_DROME	P32030	drosophila
206	6	1.8	323	1	NU1M_XENLA	P03890	xenopus lae
207	6	1.8	323	1	ZIPA_PASMU	Q9ckc8	pasteurella
208	6	1.8	324	1	KDGK_BACSU	P50845	bacillus su
209	6	1.8	326	1	RPA4_YEAST	P46669	saccharomyc
210	6	1.8	327	1	DPPF_HAEIN	P45094	haemophilus
211	6	1.8	327	1	GRHR_RAT	P30969	rattus norv
212	6	1.8	328	1	HXD1_HUMAN	Q9gzz0	homo sapien
213	6	1.8	328	1	P2Y6_HUMAN	Q15077	homo sapien
214	6	1.8	328	1	ZIPA_HAEIN	P44113	haemophilus
215	6	1.8	329	1	HEM2_SCHPO	P78974	schizosacch
216	6	1.8	334	1	DPPF_ECOLI	P37313	escherichia
217	6	1.8	336	1	SG13_CAEEL	P46567	caenorhabdi
218	6	1.8	337	1	GLK_XYLFA	Q9peg4	xylella fas
219	6	1.8	343	1	HRCA_BACSH	O69266	bacillus sp
220	6	1.8	346	1	CHEB_BACHD	Q9ka55	bacillus ha
221	6	1.8	353	1	ML1A_CHICK	P49285	gallus gall
222	6	1.8	355	1	TRPD_AZOBR	P26924	azospirillu
223	6	1.8	357	1	YFJN_ECOLI	P52129	escherichia
224	6	1.8	360	1	MK14_RAT	P70618	rattus norv
225	6	1.8	361	1	PIR3_YEAST	Q03180	saccharomyc
226	6	1.8	362	1	RLPA_ECOLI	P10100	escherichia
227	6	1.8	366	1	TGF4_HUMAN	O00292	homo sapien
228	6	1.8	369	1	Y066_NPVLD	P30325	lymantria d
229	6	1.8	373	1	AROB_CHLMU	Q9pk25	chlamydia m
230	6	1.8	373	1	Y007_METJA	Q60318	methanococc
231	6	1.8	376	1	GUNK_FUSOX	P45699	fusarium ox
232	6	1.8	376	1	VIBX_AGRT6	P09783	agrobacteri
233	6	1.8	377	1	VIBX_AGRT5	P17800	agrobacteri
234	6	1.8	377	1	VIBX_AGRT9	P05359	agrobacteri
235	6	1.8	378	1	CPCF_RABIT	P11372	oryctolagus
236	6	1.8	379	1	NLPD_ECOLI	P33648	escherichia
237	6	1.8	381	1	NAGA_HAEIN	P44537	haemophilus
238	6	1.8	385	1	CYB_STRPU	P15547	strongyloce
239	6	1.8	386	1	CRTY_ERWHE	Q01331	erwinia her
240	6	1.8	388	1	MPT1_YEAST	P50105	saccharomyc
241	6	1.8	391	1	HERP_HUMAN	Q15011	homo sapien
242	6	1.8	391	1	HERP_MOUSE	Q9jjk5	mus musculu
243	6	1.8	393	1	TCR7_VIBAN	P51563	vibrio angu
244	6	1.8	395	1	YT44_STRFR	P20188	streptomyce
245	6	1.8	396	1	A2BP_MOUSE	Q9jj43	mus musculu
246	6	1.8	397	1	A2BP_HUMAN	Q9nwb1	homo sapien
247	6	1.8	399	1	GAL1_LACLA	Q9r7d7	lactococcus
248	6	1.8	399	1	GAL1_LACLC	Q9s6s2	lactococcus
249	6	1.8	401	1	UL43_HSVEB	P28959	equine herp
250	6	1.8	406	1	ISDF_HELPY	O25664	h ispd/ispf
251	6	1.8	407	1	YAE1_SCHPO	Q09842	schizosacch
252	6	1.8	407	1	YEAD_SCHPO	O14078	schizosacch

253	6	1.8	409	1	ISDF_HELPJ	Q9zm19	h ispd/ispf
254	6	1.8	413	1	GLYA_BACHD	Q9k6g4	bacillus ha
255	6	1.8	415	1	CC11_YEAST	P32458	saccharomyc
256	6	1.8	415	1	GLYA_BACSU	P39148	bacillus su
257	6	1.8	416	1	ATTY_TRYCR	P33447	trypanosoma
258	6	1.8	416	1	GLYA_HELPY	P56089	helicobacte
259	6	1.8	416	1	MURA_BUCAI	P57466	buchnera ap
260	6	1.8	416	1	YEIJ_ECOLI	P33021	escherichia
261	6	1.8	420	1	GLYA_ACTAC	P34894	actinobacil
262	6	1.8	420	1	GLYA_PASMU	P57830	pasteurella
263	6	1.8	421	1	GLTT_BACCA	P24944	bacillus ca
264	6	1.8	421	1	GLTT_BACST	P24943	bacillus st
265	6	1.8	421	1	GLYA_HAEIN	P43844	haemophilus
266	6	1.8	423	1	YCDB_ECOLI	P31545	escherichia
267	6	1.8	426	1	AGAZ_ECOLI	P42903	escherichia
268	6	1.8	426	1	CODA_ECOLI	P25524	escherichia
269	6	1.8	426	1	GLA1_MYCTU	O53441	mycobacteri
270	6	1.8	426	1	GLYA_MYCLE	Q9x794	mycobacteri
271	6	1.8	427	1	GLYA_SYNY3	P77962	synechocyst
272	6	1.8	427	1	GLYA_THEMA	Q9wzh9	thermotoga
273	6	1.8	427	1	KDTA_HAEIN	P44806	haemophilus
274	6	1.8	428	1	DGTP_MYCSM	O52199	mycobacteri
275	6	1.8	428	1	FXB2_MOUSE	Q64733	mus musculu
276	6	1.8	428	1	GLYA_AQUAE	O66776	aquifex aeo
277	6	1.8	434	1	GLYA_HYPME	P34895	hyphomicrob
278	6	1.8	437	1	SECY_STRCO	P46785	streptomyce
279	6	1.8	437	1	SECY_STRGB	Q59912	streptomyce
280	6	1.8	437	1	SECY_STRGR	Q59916	streptomyce
281	6	1.8	437	1	SECY_STRLI	P49977	streptomyce
282	6	1.8	437	1	SECY_STRSC	P43416	streptomyce
283	6	1.8	438	1	FAS5_RHOFA	P46377	rhodococcus
284	6	1.8	439	1	COMP_BOVIN	P35445	bos taurus
285	6	1.8	440	1	SCAL_DROME	P30052	drosophila
286	6	1.8	440	1	YA33_SCHPO	Q09710	schizosacch
287	6	1.8	443	1	HXA3_HUMAN	O43365	homo sapien
288	6	1.8	445	1	ALCP_BACP3	P30145	bacillus ps
289	6	1.8	446	1	YX71_MYCTU	O50400	mycobacteri
290	6	1.8	448	1	VIME_CRIGR	P48670	cricetulus
291	6	1.8	449	1	Y753_SYNY3	P74635	synechocyst
292	6	1.8	451	1	PHT1_PSEPU	Q05181	pseudomonas
293	6	1.8	451	1	UXAC_THEMA	Q9wxr9	thermotoga
294	6	1.8	453	1	PLST_CARAU	P31393	carassius a
295	6	1.8	454	1	NFM_PIG	P08552	sus scrofa
296	6	1.8	455	1	OPSD_OCTDO	P09241	octopus dof
297	6	1.8	455	1	VIME_CYPCA	Q92155	cyprinus ca
298	6	1.8	456	1	PERI_XENLA	P48676	xenopus lae
299	6	1.8	457	1	DLDH_MYCGE	P47513	mycoplasma
300	6	1.8	457	1	KLF5_HUMAN	Q13887	homo sapien
301	6	1.8	457	1	PLSB_PEA	P30706	pisum sativ
302	6	1.8	458	1	DESM_XENLA	P23239	xenopus lae
303	6	1.8	458	1	MURA_CHLPN	Q9z7y2	chlamydia p
304	6	1.8	458	1	VIM1_XENLA	P24789	xenopus lae
305	6	1.8	459	1	VIME_CHICK	P09654	gallus gall
306	6	1.8	461	1	VIME_ONCMY	P48674	oncorhynchu
307	6	1.8	463	1	DESM_CHICK	P02542	gallus gall
308	6	1.8	463	1	VIM4_XENLA	P24790	xenopus lae
309	6	1.8	464	1	NU4M_PARLI	P12775	paracentrot
310	6	1.8	464	1	VIME_MESAU	P02544	mesocricetu
311	6	1.8	464	1	YCF1_MARPO	P12223	marchantia
312	6	1.8	465	1	VIME_BOVIN	P48616	bos taurus
313	6	1.8	465	1	VIME_HUMAN	P08670	homo sapien
314	6	1.8	465	1	VIME_MOUSE	P20152	mus musculu
315	6	1.8	465	1	VIME_RAT	P31000	rattus norv
316	6	1.8	466	1	COQ6_SCHPO	Q9y7z9	schizosacch
317	6	1.8	466	1	G3BP_HUMAN	Q13283	homo sapien
318	6	1.8	468	1	DESM_MESAU	P02541	mesocricetu
319	6	1.8	468	1	DESM_MOUSE	P31001	mus musculu
320	6	1.8	468	1	DESM_RAT	P48675	rattus norv
321	6	1.8	469	1	DESM_BOVIN	O62654	bos taurus
322	6	1.8	469	1	DESM_HUMAN	P17661	homo sapien
323	6	1.8	470	1	DESM_PIG	P02540	sus scrofa
324	6	1.8	470	1	XNIF_XENLA	P35617	xenopus lae
325	6	1.8	473	1	ARSB_RAT	P50430	rattus norv
326	6	1.8	473	1	BGLB_MICBI	P38645	microbispor
327	6	1.8	475	1	NCAP_SYNV	P10550	sonchus yel
328	6	1.8	476	1	RMUC_SALTY	Q916m7	salmonella
329	6	1.8	479	1	CBSA_SULSO	P58029	sulfolobus
330	6	1.8	480	1	SYFA_METJA	Q57911	methanococc
331	6	1.8	482	1	K2C8_RAT	Q10758	rattus norv
332	6	1.8	482	1	SECY_MYCCA	P10250	mycoplasma
333	6	1.8	485	1	LEU2_ACTTI	Q44427	actinoplane
334	6	1.8	485	1	SR54_SYNP7	Q55311	synechococc
335	6	1.8	487	1	CPC4_RABIT	P11371	oryctolagus
336	6	1.8	487	1	CPC5_RABIT	P00179	oryctolagus
337	6	1.8	487	1	CPCG_RABIT	P15123	oryctolagus
338	6	1.8	489	1	YHIP_ECOLI	P36837	escherichia
339	6	1.8	490	1	BAGT_LYMST	Q09323	lymnaea sta
340	6	1.8	490	1	CPC6_RAT	P05178	rattus norv
341	6	1.8	490	1	CPCC_RAT	P11510	rattus norv
342	6	1.8	490	1	CPCD_RAT	P20814	rattus norv
343	6	1.8	490	1	CPCP_MESAU	Q08078	mesocricetu
344	6	1.8	490	1	CPCQ_MESAU	P33263	mesocricetu
345	6	1.8	490	1	CPCR_MESAU	P33264	mesocricetu
346	6	1.8	490	1	CPCT_MOUSE	Q64458	mus musculu
347	6	1.8	490	1	CPZ3_MOUSE	P56655	mus musculu
348	6	1.8	490	1	CPZ4_MOUSE	P56656	mus musculu
349	6	1.8	491	1	CPZ5_MOUSE	P56657	mus musculu
350	6	1.8	491	1	YOJ6_CAEEL	P34629	caenorhabdi
351	6	1.8	499	1	AINX_HUMAN	Q16352	homo sapien
352	6	1.8	500	1	G6PD_SCHPO	O00091	schizosacch
353	6	1.8	501	1	TLCC_RICPR	Q9zd67	rickettsia
354	6	1.8	502	1	ACHN_HUMAN	P17787	homo sapien
355	6	1.8	502	1	DNAA_MYCLE	P46388	mycobacteri
356	6	1.8	504	1	AINX_MOUSE	P46660	mus musculu
357	6	1.8	505	1	AINX_RAT	P23565	rattus norv
358	6	1.8	508	1	CP2B_HUMAN	O15528	homo sapien
359	6	1.8	508	1	DNAA_MYCAV	P49990	mycobacteri
360	6	1.8	508	1	FTSZ_CAUCR	P52976	caulobacter
361	6	1.8	509	1	DNAA_MYCPA	Q91717	mycobacteri
362	6	1.8	509	1	STK_HYDAT	P17713	hydra atten
363	6	1.8	511	1	DHAX_HUMAN	P49419	homo sapien
364	6	1.8	513	1	SYS_METTH	O27194	methanobact
365	6	1.8	514	1	YLQ6_CAEEL	P46562	caenorhabdi
366	6	1.8	515	1	Y141_HUMAN	Q14154	homo sapien
367	6	1.8	520	1	TRPE_ECOLI	P00895	escherichia
368	6	1.8	523	1	RNFF_RHOCA	Q52718	rhodobacter
369	6	1.8	524	1	G6PI_CHLMU	Q9pk16	chlamydia m
370	6	1.8	525	1	G6PI_CHLTR	O84382	chlamydia t
371	6	1.8	526	1	4F2_MOUSE	P10852	mus musculu
372	6	1.8	526	1	G6PI_CHLPN	Q9z6n4	chlamydia p
373	6	1.8	529	1	TCPB_CAEEL	P47207	caenorhabdi
374	6	1.8	532	1	DCTS_BACHD	Q9k997	bacillus ha
375	6	1.8	532	1	YKF3_CAEEL	P34266	caenorhabdi
376	6	1.8	543	1	P2CG_BOVIN	P79126	bos taurus
377	6	1.8	544	1	SYK_METTH	O27585	methanobact
378	6	1.8	545	1	VNCS_JCDNV	Q90054	junonia coe
379	6	1.8	551	1	ETV4_HUMAN	P43268	homo sapien
380	6	1.8	552	1	YGXB_BACSU	P37874	bacillus su
381	6	1.8	554	1	HYES_MOUSE	P34914	mus musculu
382	6	1.8	555	1	ETV4_MOUSE	P28322	mus musculu
383	6	1.8	555	1	FPRB_MYCLE	O33064	mycobacteri
384	6	1.8	556	1	PRIS_THIFE	P96095	thiobacillu
385	6	1.8	557	1	G6PI_RABIT	Q9n1e2	oryctolagus
386	6	1.8	558	1	Y322_MYCGE	P47564	mycoplasma
387	6	1.8	563	1	DEAD_MYCTU	Q11039	mycobacteri
388	6	1.8	565	1	Y322_MYCPN	P75323	mycoplasma
389	6	1.8	569	1	YAP3_YEAST	P32329	saccharomyc
390	6	1.8	571	1	UGA4_YEAST	P32837	saccharomyc
391	6	1.8	574	1	LAMC_MOUSE	P11516	mus musculu
392	6	1.8	576	1	PABP_YEAST	P04147	saccharomyc
393	6	1.8	577	1	ORC2_HUMAN	Q13416	homo sapien
394	6	1.8	581	1	HEM1_STRCO	Q9wx15	streptomyce
395	6	1.8	582	1	SYN2_HUMAN	Q92777	homo sapien
396	6	1.8	583	1	LAM1_XENLA	P09010	xenopus lae
397	6	1.8	586	1	SYN2_RAT	Q63537	rattus norv
398	6	1.8	590	1	FTZ1_RHIME	P30327	rhizobium m

399	6	1.8	590	1	YKTA_CAEEL	P34322	caenorhabdi
400	6	1.8	591	1	Y875_CHLTR	O84883	chlamydia t
401	6	1.8	598	1	FLIF_PSEAE	Q51463	pseudomonas
402	6	1.8	601	1	DEAD_BUCAI	P57453	buchnera ap
403	6	1.8	601	1	HR78_DROME	Q24142	drosophila
404	6	1.8	608	1	GLMS_ECOLI	P17169	e glucosami
405	6	1.8	609	1	GLMS_PASMU	P57963	p glucosami
406	6	1.8	610	1	CDP1_ARATH	Q06850	arabidopsis
407	6	1.8	612	1	Y525_PSEAE	Q51484	pseudomonas
408	6	1.8	613	1	DEAD_HAEIN	P44586	haemophilus
409	6	1.8	615	1	SPPA_HAEIN	P45243	haemophilus
410	6	1.8	623	1	DNAK_CAMJE	O69298	campylobact
411	6	1.8	626	1	HTPG_BACSU	P46208	bacillus su
412	6	1.8	628	1	DEAD_ECOLI	P23304	escherichia
413	6	1.8	628	1	SYI_NOSLO	Q27707	nosema locu
414	6	1.8	636	1	GYRB_THEMA	P77993	thermotoga
415	6	1.8	637	1	YHW1_YEAST	P38856	saccharomyc
416	6	1.8	639	1	LACY_LEULA	Q48624	leuconostoc
417	6	1.8	642	1	DEAD_KLEPN	P33906	klebsiella
418	6	1.8	642	1	DNAK_FRATU	P48205	francisella
419	6	1.8	643	1	GAG_SFV3L	P27400	simian foam
420	6	1.8	643	1	YNV4_CAEEL	P34567	caenorhabdi
421	6	1.8	644	1	NFM_RABIT	P54938	oryctolagus
422	6	1.8	646	1	NA95_HUMAN	Q9ulx6	homo sapien
423	6	1.8	647	1	VE1_HPV52	P36730	human papil
424	6	1.8	657	1	LAMA_CHICK	P13648	gallus gall
425	6	1.8	664	1	LAMA_HUMAN	P02545	homo sapien
426	6	1.8	665	1	LAMA_MOUSE	P48678	mus musculu
427	6	1.8	665	1	LAMA_RAT	P48679	rattus norv
428	6	1.8	665	1	LAMA_XENLA	P11048	xenopus lae
429	6	1.8	672	1	HMW3_MYCPN	Q50360	mycoplasma
430	6	1.8	679	1	MTO1_YEAST	P53070	saccharomyc
431	6	1.8	683	1	BGH3_HUMAN	Q15582	homo sapien
432	6	1.8	685	1	SC31_HUMAN	Q07837	homo sapien
433	6	1.8	694	1	VGLH_HSV6U	P30001	human herpe
434	6	1.8	694	1	VGLH_HSV6Z	P52543	human herpe
435	6	1.8	699	1	E75_MANSE	Q08893	manduca sex
436	6	1.8	704	1	HS85_TRYCR	P06660	trypanosoma
437	6	1.8	705	1	ADDG_RAT	Q62847	rattus norv
438	6	1.8	705	1	MMLD_STRCO	Q9xa86	streptomyce
439	6	1.8	706	1	ADDG_MOUSE	Q9qyb5	mus musculu
440	6	1.8	707	1	NU5C_MALAR	Q9mvl6	malvaviscus
441	6	1.8	709	1	NU5C_PACAQ	Q9mvk2	pachira aqu
442	6	1.8	711	1	E75_GALME	P50239	galleria me
443	6	1.8	714	1	PILQ_PSEAE	P34750	pseudomonas
444	6	1.8	716	1	IKKE_HUMAN	Q14164	homo sapien
445	6	1.8	717	1	IKKE_MOUSE	Q9r0t8	mus musculu
446	6	1.8	717	1	NAH4_RAT	P26434	rattus norv
447	6	1.8	717	1	TRD1_ECOLI	P09130	escherichia
448	6	1.8	718	1	YSO2_CAEEL	Q10128	caenorhabdi
449	6	1.8	722	1	HMN2_DROME	P22808	drosophila
450	6	1.8	723	1	HR96_DROME	Q24143	drosophila
451	6	1.8	732	1	PSAA_HETTR	Q9xqv3	heterocapsa
452	6	1.8	744	1	RELA_ECOLI	P11585	escherichia
453	6	1.8	753	1	METE_SALTY	Q916n1	salmonella
454	6	1.8	755	1	COMP_RAT	P35444	rattus norv
455	6	1.8	757	1	COMP_HUMAN	P49747	homo sapien
456	6	1.8	761	1	NETR_MOUSE	O08762	mus musculu
457	6	1.8	765	1	AOC3_MOUSE	O70423	mus musculu
458	6	1.8	766	1	SAK1_SCHPO	P48383	schizosacch
459	6	1.8	769	1	ITB2_BOVIN	P32592	bos taurus
460	6	1.8	769	1	ITB2_PIG	P53714	sus scrofa
461	6	1.8	770	1	A4_MOUSE	P12023	mus musculu
462	6	1.8	770	1	A4_RAT	P08592	rattus norv
463	6	1.8	774	1	RRP3_INCBE	P21770	influenza c
464	6	1.8	774	1	RRP3_INCJJ	P13877	influenza c
465	6	1.8	778	1	FTSK_COXBU	P39920	coxiella bu
466	6	1.8	781	1	GCS1_CAEEL	Q19426	caenorhabdi
467	6	1.8	785	1	YHY2_YEAST	P38870	saccharomyc
468	6	1.8	798	1	UNR_HUMAN	O75534	homo sapien
469	6	1.8	798	1	UNR_RAT	P18395	rattus norv
470	6	1.8	802	1	ACSB_ACEXY	P37716	acetobacter
471	6	1.8	810	1	NFM_BOVIN	O77788	bos taurus
472	6	1.8	811	1	MUTS_THEAQ	Q56215	thermus aqu
473	6	1.8	817	1	MUTS_THECA	Q9zix6	thermus aqu
474	6	1.8	818	1	MUTS_THETH	Q56239	thermus aqu
475	6	1.8	830	1	PKN2_MYXXA	P54736	myxococcus
476	6	1.8	831	1	NFH_RAT	P16884	rattus norv
477	6	1.8	837	1	LDLR_RABIT	P20063	oryctolagus
478	6	1.8	845	1	NFM_RAT	P12839	rattus norv
479	6	1.8	848	1	NFM_MOUSE	P08553	mus musculu
480	6	1.8	849	1	PR05_YEAST	P21372	saccharomyc
481	6	1.8	853	1	NUG2_RHIME	P56914	rhizobium m
482	6	1.8	857	1	NFM_CHICK	P16053	gallus gall
483	6	1.8	859	1	DD24_HUMAN	Q9gzr7	homo sapien
484	6	1.8	859	1	YD48_MYCTU	Q11018	mycobacteri
485	6	1.8	901	1	DSC2_HUMAN	Q02487	homo sapien
486	6	1.8	901	1	PIP_LACLA	P49022	lactococcus
487	6	1.8	902	1	EPBB_XENLA	Q91736	xenopus lae
488	6	1.8	904	1	SECA_RHOCA	P52966	rhodobacter
489	6	1.8	907	1	NUOG_ECOLI	P33602	escherichia
490	6	1.8	907	1	NUOG_SALTY	P33900	salmonella
491	6	1.8	910	1	PERT_BORPE	P14283	bordetella
492	6	1.8	911	1	PERT_BORBR	Q03035	bordetella
493	6	1.8	915	1	NFM_HUMAN	P07197	homo sapien
494	6	1.8	922	1	PERT_BORPA	P24328	bordetella
495	6	1.8	936	1	CAPP_RHOPA	O32483	rhodopseudo
496	6	1.8	937	1	A2B1_HUMAN	P21851	homo sapien
497	6	1.8	939	1	YL09_YEAST	Q06078	saccharomyc
498	6	1.8	950	1	UVRA_NEIGO	Q50968	neisseria g
499	6	1.8	955	1	TSP4_XENLA	Q06441	xenopus lae
500	6	1.8	956	1	YEF3_YEAST	P32618	saccharomyc
501	6	1.8	961	1	TSP4_HUMAN	P35443	homo sapien
502	6	1.8	968	1	BCA1_RAT	Q63767	rattus norv
503	6	1.8	969	1	DPOM_NEUIN	P33538	neurospora
504	6	1.8	971	1	Y029_HUMAN	Q15032	homo sapien
505	6	1.8	979	1	PTPN_MOUSE	Q60673	mus musculu
506	6	1.8	980	1	TSP4_RAT	P49744	rattus norv
507	6	1.8	983	1	Y144_HUMAN	Q14157	homo sapien
508	6	1.8	984	1	EPB1_CHICK	Q07494	gallus gall
509	6	1.8	984	1	EPB1_HUMAN	P54762	homo sapien
510	6	1.8	984	1	EPB1_RAT	P09759	rattus norv
511	6	1.8	986	1	DPO1_SYNY3	Q55971	synechocyst
512	6	1.8	986	1	GM13_RAT	Q62839	rattus norv
513	6	1.8	1018	1	DPOG_SCHPO	Q12704	schizosacch
514	6	1.8	1018	1	HIRA_CHICK	P79987	gallus gall
515	6	1.8	1020	1	NFH_HUMAN	P12036	homo sapien
516	6	1.8	1027	1	ISWI_DROME	Q24368	drosophila
517	6	1.8	1030	1	SPAB_BACSU	P39774	bacillus su
518	6	1.8	1039	1	Y4JQ_RHISN	P55517	rhizobium s
519	6	1.8	1043	1	CHS2_PARBR	Q92444	paracoccidi
520	6	1.8	1064	1	SYI_AERPE	Q9yf67	aeropyrum p
521	6	1.8	1069	1	RNT1_CAEEL	O76512	caenorhabdi
522	6	1.8	1084	1	HDA4_HUMAN	P56524	homo sapien
523	6	1.8	1087	1	NFH_MOUSE	P19246	mus musculu
524	6	1.8	1092	1	LIFR_MOUSE	P42703	mus musculu
525	6	1.8	1096	1	KPC1_ASPNG	Q00078	aspergillus
526	6	1.8	1114	1	TCF8_CHICK	P36197	gallus gall
527	6	1.8	1118	1	UBP8_HUMAN	P40818	homo sapien
528	6	1.8	1123	1	V120_HSV11	P10221	herpes simp
529	6	1.8	1157	1	Y182_HUMAN	Q14687	homo sapien
530	6	1.8	1173	1	DPOL_RCMVM	Q85428	rat cytomeg
531	6	1.8	1211	1	DP3A_HELPJ	Q9zjf9	helicobacte
532	6	1.8	1211	1	DP3A_HELPY	P56157	helicobacte
533	6	1.8	1225	1	VGL2_CVPR8	P27655	porcine res
534	6	1.8	1225	1	VGL2_CVPRM	P24413	porcine res
535	6	1.8	1231	1	BLM_CAEEL	O18017	caenorhabdi
536	6	1.8	1247	1	POLS_ONNVG	P22056	o'nyong-nyo
537	6	1.8	1256	1	ATL_STAAU	P52081	staphylococ
538	6	1.8	1257	1	PER2_MOUSE	O54943	mus musculu
539	6	1.8	1262	1	CA13_CHICK	P12105	gallus gall
540	6	1.8	1270	1	VGLN_CHICK	P81021	gallus gall
541	6	1.8	1297	1	PUR4_VIBCH	Q9ktn2	vibrio chol
542	6	1.8	1302	1	UBPY_CAEEL	Q09931	caenorhabdi
543	6	1.8	1317	1	YAOF_SCHPO	Q10094	schizosacch
544	6	1.8	1329	1	FTSK_ECOLI	P46889	escherichia

545	6	1.8	1331	1	CTA2_HUMAN	Q9uhc6	homo sapien
546	6	1.8	1332	1	XKDO_BACSU	P54334	bacillus su
547	6	1.8	1335	1	XDH_DROME	P10351	drosophila
548	6	1.8	1365	1	SUZ2_DROME	P25172	drosophila
549	6	1.8	1381	1	CTA1_RAT	P97846	rattus norv
550	6	1.8	1384	1	CTA1_HUMAN	P78357	homo sapien
551	6	1.8	1385	1	CTA1_MOUSE	O54991	mus musculu
552	6	1.8	1425	1	MADI_HUMAN	O95405	homo sapien
553	6	1.8	1440	1	SYEP_HUMAN	P07814	homo sapien
554	6	1.8	1441	1	VGLM_BUNL7	P09612	bunyavirus
555	6	1.8	1447	1	VGL2_CVPPR	Q02167	porcine tra
556	6	1.8	1447	1	VGL2_CVPPU	P07946	porcine tra
557	6	1.8	1447	1	VGL2_CVPRT	Q01977	porcine tra
558	6	1.8	1449	1	VGL2_CVPFS	P18450	porcine tra
559	6	1.8	1449	1	VGL2_CVPMI	P33470	porcine tra
560	6	1.8	1451	1	VGL2_CVCAI	P36300	canine ente
561	6	1.8	1452	1	VGL2_FIPV	P10033	feline infe
562	6	1.8	1461	1	TOP2_CANAL	P87078	candida alb
563	6	1.8	1676	1	APSA_EMENI	Q00083	emericella
564	6	1.8	1687	1	CCAM_MUSDO	Q25452	musca domes
565	6	1.8	1691	1	YLH4_CAEEL	P34358	caenorhabdi
566	6	1.8	1701	1	U520_HUMAN	O75643	homo sapien
567	6	1.8	1744	1	TENS_CHICK	Q04205	gallus gall
568	6	1.8	1745	1	ZO1_MOUSE	P39447	mus musculu
569	6	1.8	1772	1	MSP1_PLAYO	P13828	plasmodium
570	6	1.8	1794	1	YAV1_SCHPO	Q10172	schizosacch
571	6	1.8	1816	1	AF6_HUMAN	P55196	homo sapien
572	6	1.8	1862	1	ANK1_MOUSE	Q02357	mus musculu
573	6	1.8	2226	1	POLG_HPAV2	P26580	hepatitis a
574	6	1.8	2226	1	POLG_HPAV4	P26581	hepatitis a
575	6	1.8	2226	1	POLG_HPAV8	P26582	hepatitis a
576	6	1.8	2227	1	POLG_HPAVH	P08617	hepatitis a
577	6	1.8	2227	1	POLG_HPAVL	P06441	hepatitis a
578	6	1.8	2227	1	POLG_HPAVM	P13901	hepatitis a
579	6	1.8	2230	1	POLG_HPAVS	P14553	simian hepa
580	6	1.8	2333	1	POLG_FMDV1	P03306	f genome po
581	6	1.8	2397	1	MOKB_SCHPO	Q09854	schizosacch
582	6	1.8	2469	1	TEGU_HSVSA	Q01056	herpesvirus
583	6	1.8	2482	1	VWF_PIG	Q28833	sus scrofa
584	6	1.8	2515	1	TUD_DROME	P25823	drosophila
585	6	1.8	2516	1	CCAD_DROME	Q24270	drosophila
586	6	1.8	3149	1	TEGU_EBV	P03186	epstein-bar
587	6	1.8	3411	1	POLG_YEFV1	P03314	y genome po
588	6	1.8	3411	1	POLG_YEFV2	P19901	y genome po
589	6	1.8	3415	1	POLG_POWVL	Q04538	t genome po
590	6	1.8	3418	1	BRC2_HUMAN	P51587	homo sapien
591	6	1.8	3672	1	LML2_CAEEL	Q21313	caenorhabdi
592	6	1.8	3695	1	LMA5_HUMAN	O15230	homo sapien
593	6	1.8	3726	1	ABF1_MOUSE	Q61329	mus musculu
594	6	1.8	3828	1	TRX_DROVI	Q24742	drosophila
595	6	1.8	4543	1	LRP1_CHICK	P98157	gallus gall
596	5	1.5	11	1	ULAG_HUMAN	P31933	homo sapien
597	5	1.5	15	1	PDGB_PIG	P20034	sus scrofa
598	5	1.5	18	1	SFAH_HELAN	P81098	helianthus
599	5	1.5	21	1	TKNC_CARAU	P25421	carassius a
600	5	1.5	34	1	COL_CHICK	P11148	gallus gall
601	5	1.5	37	1	PRF1_RAT	P18889	rattus norv
602	5	1.5	40	1	PMP1_YEAST	P32903	saccharomyc
603	5	1.5	42	1	COAT_BPPHL	Q07485	bacteriopha
604	5	1.5	43	1	PSBF_SYNY3	P09191	synechocyst
605	5	1.5	45	1	TRXB_VIBFI	P80892	vibrio fisc
606	5	1.5	46	1	LHB1_RHOPA	P35106	rhodopseudo
607	5	1.5	48	1	POPI_BOVIN	P01154	bos taurus
608	5	1.5	50	1	LHB2_RHOPA	P35107	rhodopseudo
609	5	1.5	51	1	INS_PLAFE	P09477	platichthys
610	5	1.5	52	1	GLP_CANFA	P02727	canis famil
611	5	1.5	52	1	NU3M_NEUCR	Q35141	neurospora
612	5	1.5	52	1	RUBR_DESVH	P00269	desulfovibr
613	5	1.5	52	1	RUBR_DESVM	P15412	desulfovibr
614	5	1.5	53	1	LHA1_RHOAC	P35089	rhodopseudo
615	5	1.5	53	1	LHA2_RHOAC	P35090	rhodopseudo
616	5	1.5	55	1	ATP8_PELSU	O79674	pelomedusa
617	5	1.5	55	1	FER_CLOST	P80168	clostridium
618	5	1.5	55	1	V6K_BYDVP	P09518	barley yell
619	5	1.5	57	1	A4_PIG	Q29023	sus scrofa
620	5	1.5	57	1	A4_URSMA	Q29149	ursus marit
621	5	1.5	58	1	A4_CANFA	Q28280	canis famil
622	5	1.5	58	1	A4_RABIT	Q28748	oryctolagus
623	5	1.5	58	1	A4_SHEEP	Q28757	ovis aries
624	5	1.5	59	1	A4_BOVIN	Q28053	bos taurus
625	5	1.5	60	1	RL32_DEIRA	P49228	deinococcus
626	5	1.5	60	1	RS21_SYNY3	P48949	synechocyst
627	5	1.5	61	1	YVDH_VACCV	P04316	vaccinia vi
628	5	1.5	62	1	COXS_MOUSE	P56394	mus musculu
629	5	1.5	62	1	STAT_HUMAN	P02808	homo sapien
630	5	1.5	62	1	YZ05_METJA	Q60262	methanococc
631	5	1.5	64	1	BCNB_CLOPE	P15936	clostridium
632	5	1.5	66	1	YSCE_YEREN	Q01246	yersinia en
633	5	1.5	68	1	NLT2_PRUAR	P82353	prunus arme
634	5	1.5	68	1	S61G_CAEEL	Q19967	caenorhabdi
635	5	1.5	68	1	YRP3_AZOCA	P33988	azorhizobiu
636	5	1.5	71	1	CER1_CERCA	P36190	ceratitis c
637	5	1.5	71	1	CER2_CERCA	O17512	ceratitis c
638	5	1.5	74	1	MCPB_BOVIN	P80343	bos taurus
639	5	1.5	74	1	YC47_ODOSI	P49542	odontella s
640	5	1.5	75	1	PSK_ASPOF	Q9fs10	asparagus o
641	5	1.5	75	1	S100_LEPPA	P82978	lepidosiren
642	5	1.5	77	1	PSK5_ARATH	Q9feb4	arabidopsis
643	5	1.5	77	1	RUXG_YEAST	P40204	saccharomyc
644	5	1.5	77	1	YAML_STRVL	P23822	streptomyce
645	5	1.5	78	1	Y055_TREPA	O83094	treponema p
646	5	1.5	78	1	Y150_UREPA	Q9pqz4	ureaplasma
647	5	1.5	78	1	YPJK_ECOLI	P52134	escherichia
648	5	1.5	79	1	DEF1_STOCA	O16136	stomoxys ca
649	5	1.5	79	1	NU5M_LEMCA	Q34879	lemur catta
650	5	1.5	79	1	YE09_STRCO	O69880	streptomyce
651	5	1.5	80	1	AFP1_BRANA	P30225	brassica na
652	5	1.5	81	1	Y00H_BPT4	P39418	bacteriopha
653	5	1.5	81	1	Y334_ARCFU	O29913	archaeoglob
654	5	1.5	81	1	YMJA_ECOLI	P76036	escherichia
655	5	1.5	81	1	YO02_BPL2	P42537	bacteriopha
656	5	1.5	82	1	HFQ_PSEAE	Q9hum0	pseudomonas
657	5	1.5	82	1	MLC1_DROMA	Q24399	drosophila
658	5	1.5	82	1	MLC1_DROSE	Q24656	drosophila
659	5	1.5	82	1	MLC1_DROTE	Q24695	drosophila
660	5	1.5	82	1	MLC1_DROYA	Q24766	drosophila
661	5	1.5	83	1	HPIS_THETI	P80176	thermochrom
662	5	1.5	83	1	Y67_BPT3	P20330	bacteriopha
663	5	1.5	85	1	BM02_HUMAN	Q9nzf2	homo sapien
664	5	1.5	85	1	BM02_MOUSE	Q9cpx2	mus musculu
665	5	1.5	85	1	HPIS_THIRO	P00261	thiocapsa r
666	5	1.5	85	1	Y12K_MSVS	P14993	maize strea
667	5	1.5	86	1	OAG1_VIBCH	Q9kuh2	vibrio chol
668	5	1.5	86	1	R31B_STRPY	Q9a016	streptococc
669	5	1.5	86	1	REV_HV1Z3	P05867	human immun
670	5	1.5	86	1	RS17_BACHD	Q9z9k5	bacillus ha
671	5	1.5	86	1	RS17_BACSU	P12874	bacillus su
672	5	1.5	86	1	RS17_STRPN	Q9ww03	streptococc
673	5	1.5	86	1	VE7_HPV10	P36818	human papil
674	5	1.5	87	1	RS20_ZYMMO	Q9z5v0	zymomonas m
675	5	1.5	87	1	VE7_HPV28	P50783	human papil
676	5	1.5	88	1	ATPE_CHLLI	P35111	chlorobium
677	5	1.5	88	1	COXM_BOVIN	P13183	bos taurus
678	5	1.5	88	1	CU70_LOCMI	P80232	locusta mig
679	5	1.5	88	1	EF1B_THEAC	Q9hkn1	thermoplasm
680	5	1.5	88	1	Y4BB_RHISN	P55369	rhizobium s
681	5	1.5	88	1	Y4OL_RHISN	P55597	rhizobium s
682	5	1.5	89	1	FLIQ_BACSU	P35535	bacillus su
683	5	1.5	89	1	IM9A_HUMAN	Q9y5j7	homo sapien
684	5	1.5	89	1	IM9A_MOUSE	Q9wv98	mus musculu
685	5	1.5	89	1	SLTB_BP933	P09386	bacteriopha
686	5	1.5	89	1	XHLA_BACSU	P39798	bacillus su
687	5	1.5	89	1	YCO2_PARDE	P08302	paracoccus
688	5	1.5	90	1	PTSO_PROMI	Q9za86	proteus mir
689	5	1.5	90	1	VE7_HPV29	P50784	human papil
690	5	1.5	92	1	IM13_DROME	Q9vtn3	drosophila

691	5	1.5	92	1	SP12_ARATH	Q944j0	arabidopsis
692	5	1.5	92	1	YC23_METJA	Q58620	methanococc
693	5	1.5	92	1	YPS1_SYNP2	P31525	synechococc
694	5	1.5	92	1	YRI3_CORAM	Q45825	corynebacte
695	5	1.5	93	1	NODF_RHIME	P06232	rhizobium m
696	5	1.5	93	1	U185_ARATH	Q9ca23	arabidopsis
697	5	1.5	93	1	YQIC_CAEEL	Q09283	caenorhabdi
698	5	1.5	94	1	YBJH_ECOLI	P75808	escherichia
699	5	1.5	94	1	YOY3_CAEEL	P34661	caenorhabdi
700	5	1.5	95	1	DBH_THETH	P19436	thermus aqu
701	5	1.5	95	1	I13A_HUMAN	Q9uhl8	homo sapien
702	5	1.5	95	1	I13B_HUMAN	Q9y514	homo sapien
703	5	1.5	95	1	R37A_HALN1	Q9hsg8	halobacteri
704	5	1.5	95	1	RL23_BACST	P04454	bacillus st
705	5	1.5	95	1	RR20_CYAPA	P48140	cyanophora
706	5	1.5	95	1	YVBC_VACCC	P20543	vaccinia vi
707	5	1.5	95	1	YY1_ORYSA	O23810	oryza sativ
708	5	1.5	96	1	CATC_ACICA	Q43932	acinetobact
709	5	1.5	96	1	RT24_SCHPO	O43020	schizosacch
710	5	1.5	96	1	U185_CHLRE	Q94ey2	chlamydomon
711	5	1.5	96	1	VE7_HPV60	Q80942	human papil
712	5	1.5	97	1	DEF4_HUMAN	P12838	homo sapien
713	5	1.5	97	1	HFQ_NEIMA	Q9jqw6	neisseria m
714	5	1.5	97	1	NO75_MEDSA	P11728	medicago sa
715	5	1.5	98	1	CYTB_HUMAN	P04080	homo sapien
716	5	1.5	98	1	Z126_HUMAN	P35275	homo sapien
717	5	1.5	99	1	IHFA_PASHA	P95516	pasteurella
718	5	1.5	99	1	MCPA_BOVIN	P28291	bos taurus
719	5	1.5	99	1	SY02_HUMAN	P13500	homo sapien
720	5	1.5	99	1	SY02_MACFA	Q9myn4	macaca fasc
721	5	1.5	99	1	SY02_PIG	P42831	sus scrofa
722	5	1.5	99	1	SY08_HUMAN	P80075	homo sapien
723	5	1.5	100	1	BPT2_BOVIN	P04815	bos taurus
724	5	1.5	100	1	RR18_PINTH	P52763	pinus thunb
725	5	1.5	100	1	V07K_NMV	P15098	narcissus m
726	5	1.5	100	1	Y151_ARCFU	O30086	archaeoglob
727	5	1.5	100	1	Y908_HAEIN	P44073	haemophilus
728	5	1.5	100	1	YC83_ARCFU	O28985	archaeoglob
729	5	1.5	101	1	CH10_HUMAN	Q04984	homo sapien
730	5	1.5	101	1	CH10_MOUSE	Q64433	mus musculu
731	5	1.5	101	1	CH10_RAT	P26772	rattus norv
732	5	1.5	101	1	SY02_CANFA	P52203	canis famil
733	5	1.5	101	1	THYP_HUMAN	P20962	homo sapien
734	5	1.5	101	1	Y941_HAEIN	P44082	haemophilus
735	5	1.5	101	1	YD31_MYCTU	Q10642	mycobacteri
736	5	1.5	102	1	ATPN_BOVIN	Q28852	bos taurus
737	5	1.5	102	1	U185_ORYSA	Q94dm8	oryza sativ
738	5	1.5	102	1	Y12K_MSVN	P14974	maize strea
739	5	1.5	102	1	YI98_MYCTU	O07734	mycobacteri
740	5	1.5	102	1	YMSA_RHIME	Q07602	rhizobium m
741	5	1.5	103	1	YLK4_CAEEL	P41952	caenorhabdi
742	5	1.5	104	1	ARTA_ECOLI	P18032	escherichia
743	5	1.5	104	1	METJ_ECOLI	P08338	escherichia
744	5	1.5	104	1	METJ_SALTY	P06203	salmonella
745	5	1.5	104	1	UGR2_MOUSE	Q920d7	mus musculu
746	5	1.5	104	1	YDTD_SCHPO	O14218	schizosacch
747	5	1.5	104	1	YJB8_YEAST	P47070	saccharomyc
748	5	1.5	104	1	YQ11_BACAN	Q9rn21	bacillus an
749	5	1.5	105	1	YKKD_BACSU	P49857	bacillus su
750	5	1.5	106	1	GUAU_MOUSE	O09051	mus musculu
751	5	1.5	106	1	GUAU_RAT	P70668	rattus norv
752	5	1.5	106	1	ILB2_CAEEL	Q09627	caenorhabdi
753	5	1.5	106	1	PRVB_LEUCE	P05939	leuciscus c
754	5	1.5	106	1	Y4VC_RHISN	Q53211	rhizobium s
755	5	1.5	106	1	Y952_CAUCR	Q45979	caulobacter
756	5	1.5	107	1	MTC2_HUMAN	P56278	homo sapien
757	5	1.5	107	1	PER_BERVA	Q17285	beris valla
758	5	1.5	107	1	QACC_STAAU	P14319	staphylococ
759	5	1.5	107	1	QACC_STASP	Q55339	staphylococ
760	5	1.5	107	1	RT24_NEUCR	P08580	neurospora
761	5	1.5	107	1	U139_ARATH	Q9sd88	arabidopsis
762	5	1.5	107	1	YJM0_YEAST	P47020	saccharomyc
763	5	1.5	108	1	INS1_MOUSE	P01325	mus musculu
764	5	1.5	108	1	PRVB_CYPCA	P02618	cyprinus ca
765	5	1.5	108	1	Y826_RICPR	Q9zcd1	rickettsia
766	5	1.5	108	1	YC54_PORPU	P51204	porphyra pu
767	5	1.5	108	1	YD31_MYCLE	P53423	mycobacteri
768	5	1.5	109	1	HMGC_HUMAN	P52926	homo sapien
769	5	1.5	109	1	NUOM_HUMAN	P56181	homo sapien
770	5	1.5	109	1	PRVA_TRISE	P30563	triakis sem
771	5	1.5	109	1	R31B_CHLPN	Q9z969	chlamydia p
772	5	1.5	109	1	YIR1_YEAST	P40440	saccharomyc
773	5	1.5	109	1	YX_BACSH	P39044	bacillus sp
774	5	1.5	110	1	CYOD_PSEPU	Q9wwr4	pseudomonas
775	5	1.5	110	1	HMGB_CHITE	P40623	chironomus
776	5	1.5	110	1	PEPA_BOVIN	P00792	bos taurus
777	5	1.5	110	1	RLA4_SCHPO	P17478	schizosacch
778	5	1.5	111	1	FLIE_BORBU	P52609	borrelia bu
779	5	1.5	111	1	PHNA_ECOLI	P16680	escherichia
780	5	1.5	111	1	RLA1_CAEEL	P91913	caenorhabdi
781	5	1.5	111	1	VE7_HPV07	P36816	human papil
782	5	1.5	112	1	CORT_RAT	Q62949	rattus norv
783	5	1.5	112	1	GLNB_AQUAE	O66513	aquifex aeo
784	5	1.5	112	1	HMGD_DROME	Q05783	drosophila
785	5	1.5	112	1	YBAV_HAEIN	Q57134	haemophilus
786	5	1.5	112	1	YFIA_ECOLI	P11285	escherichia
787	5	1.5	113	1	H38_STYLE	P81202	stylonychia
788	5	1.5	113	1	HYBF_KLEPN	Q9f0d4	klebsiella
789	5	1.5	113	1	HYBF_MORMO	Q9zhr1	morganella
790	5	1.5	113	1	LCCI_LEUGE	P34035	leuconostoc
791	5	1.5	113	1	REV_HV1J3	P12484	human immun
792	5	1.5	113	1	YC71_MYCTU	Q11048	mycobacteri
793	5	1.5	114	1	YEJG_ECOLI	P33917	escherichia
794	5	1.5	114	1	YGAC_ECOLI	P36931	escherichia
795	5	1.5	114	1	YZ11_METJA	Q60273	methanococc
796	5	1.5	115	1	MQO_KLEPN	O32719	klebsiella
797	5	1.5	115	1	REV_HV1MN	P05871	human immun
798	5	1.5	115	1	RLA2_HUMAN	P05387	homo sapien
799	5	1.5	115	1	RLA2_PIG	Q29315	sus scrofa
800	5	1.5	115	1	RLA2_RAT	P02401	rattus norv
801	5	1.5	115	1	Y4HO_RHISN	P50359	rhizobium s
802	5	1.5	115	1	YIDH_ECOLI	P31445	escherichia
803	5	1.5	115	1	YXEA_BACSU	P54940	bacillus su
804	5	1.5	116	1	NU3M_CHICK	P18938	gallus gall
805	5	1.5	116	1	NU3M_LATCH	O03171	latimeria c
806	5	1.5	116	1	REV_HV1JR	P20869	human immun
807	5	1.5	116	1	VXIS_BPP22	P04889	bacteriopha
808	5	1.5	117	1	GSPI_VIBCH	P45775	vibrio chol
809	5	1.5	117	1	NU3M_LUMTE	Q34950	lumbricus t
810	5	1.5	117	1	NU3M_PLASU	Q36518	platymonas
811	5	1.5	117	1	VATG_MANSE	Q25532	manduca sex
812	5	1.5	117	1	Y4NH_RHISN	P55580	rhizobium s
813	5	1.5	118	1	REV_HV1EL	P04621	human immun
814	5	1.5	118	1	THH5_ARATH	Q39241	arabidopsis
815	5	1.5	118	1	TRH4_ECOLI	Q00190	escherichia
816	5	1.5	118	1	Y493_HAEIN	O05023	haemophilus
817	5	1.5	118	1	Y914_AQUAE	O67059	aquifex aeo
818	5	1.5	118	1	YFFB_ECOLI	P24178	escherichia
819	5	1.5	118	1	YHAI_ECOLI	P42622	escherichia
820	5	1.5	118	1	YRB2_CAEEL	Q09399	caenorhabdi
821	5	1.5	119	1	ANTA_HAEGH	P16242	haementeria
822	5	1.5	119	1	B2MG_CALTO	O77530	callicebus
823	5	1.5	119	1	HV2C_HUMAN	P01816	homo sapien
824	5	1.5	119	1	ID3_HUMAN	Q02535	homo sapien
825	5	1.5	119	1	ID3_MOUSE	P41133	mus musculu
826	5	1.5	119	1	ID3_RAT	P41138	rattus norv
827	5	1.5	119	1	ML1X_RAT	Q62953	rattus norv
828	5	1.5	119	1	PYHD_NPVAP	P41711	antheraea p
829	5	1.5	119	1	THH2_BRANA	Q39362	brassica na
830	5	1.5	119	1	YQ06_PSEAE	Q9i0n2	pseudomonas
831	5	1.5	120	1	C550_BACSU	P24469	bacillus su
832	5	1.5	120	1	FOLB_BACSU	P28823	bacillus su
833	5	1.5	120	1	HV2B_HUMAN	P01815	homo sapien
834	5	1.5	120	1	NU3C_MARPO	P06259	marchantia
835	5	1.5	120	1	NU3C_TOBAC	P06258	nicotiana t
836	5	1.5	120	1	SY16_HUMAN	O15467	homo sapien

837	5	1.5	121	1	CH15_DROSU	P13426	drosophila
838	5	1.5	121	1	FLIT_ECOLI	P26610	escherichia
839	5	1.5	121	1	PA22_CERGO	P81165	cerrophidio
840	5	1.5	121	1	RNPA_NEIMB	Q9jxs6	neisseria m
841	5	1.5	121	1	YC84_METJA	Q58680	methanococc
842	5	1.5	121	1	YCF2_VICFA	P15821	vicia faba
843	5	1.5	122	1	HPIS_CHRVI	P00260	chromatium
844	5	1.5	122	1	HV3G_HUMAN	P01768	homo sapien
845	5	1.5	122	1	INL3_MOUSE	O09107	mus musculu
846	5	1.5	122	1	MPI3_LYMST	P80090	lymnaea sta
847	5	1.5	123	1	CRCB_PYRHO	O59171	pyrococcus
848	5	1.5	123	1	REV_HV1U4	P24739	human immun
849	5	1.5	124	1	CRCB_RHILO	Q98n26	rhizobium l
850	5	1.5	124	1	PRO1_PHYPO	P22271	physarum po
851	5	1.5	124	1	RIBT_BACSU	P17622	bacillus su
852	5	1.5	124	1	SP0F_BACSU	P06628	bacillus su
853	5	1.5	124	1	VATF_NEUCR	Q9y756	neurospora
854	5	1.5	124	1	YB28_YEAST	P38296	saccharomyc
855	5	1.5	124	1	YC69_MYCTU	Q11050	mycobacteri
856	5	1.5	124	1	YHCC_BACSU	P54587	bacillus su
857	5	1.5	125	1	GLHA_FUNHE	P47744	fundulus he
858	5	1.5	125	1	PFDB_HALN1	Q9hsh0	halobacteri
859	5	1.5	125	1	PYP_CHRSA	P81046	chromatium
860	5	1.5	125	1	SY02_RABIT	P28292	oryctolagus
861	5	1.5	125	1	SYB_LOLPE	P47194	loligo peal
862	5	1.5	126	1	C10_MOUSE	O35127	mus musculu
863	5	1.5	126	1	HV2A_HUMAN	P01814	homo sapien
864	5	1.5	126	1	YYAH_BACSU	P37516	bacillus su
865	5	1.5	127	1	CYCP_ALCXX	P00138	alcaligenes
866	5	1.5	127	1	NIK1_METTH	O26703	methanobact
867	5	1.5	127	1	RT08_ACACA	P46757	acanthamoeb
868	5	1.5	127	1	SPG1_DICDI	P15519	dictyosteli
869	5	1.5	127	1	SPG2_DICDI	P15520	dictyosteli
870	5	1.5	127	1	SPG3_DICDI	P15521	dictyosteli
871	5	1.5	127	1	Y4KH_RHISN	P55528	rhizobium s
872	5	1.5	128	1	CUER_HAEIN	P44617	haemophilus
873	5	1.5	128	1	LSHB_STRCA	P80664	struthio ca
874	5	1.5	128	1	RBFA_HAEIN	P45141	haemophilus
875	5	1.5	128	1	RS9_THETH	P80374	thermus aqu
876	5	1.5	128	1	Y070_TREPA	O83109	treponema p
877	5	1.5	129	1	DYL4_CHLRE	Q39591	chlamydomon
878	5	1.5	129	1	IHFA_MYXXA	Q9k4q3	myxococcus
879	5	1.5	129	1	VAL2_ABMVW	P21944	abutilon mo
880	5	1.5	129	1	VAL2_TGMV	P03562	tomato gold
881	5	1.5	129	1	VAL2_TMOV	Q06658	tomato mott
882	5	1.5	129	1	VH07_VACCV	P08586	vaccinia vi
883	5	1.5	129	1	Y207_AERPE	Q9yfp2	aeropyrum p
884	5	1.5	129	1	YAER_ECOLI	P52096	escherichia
885	5	1.5	130	1	ACPS_MYCLE	Q9x7e3	mycobacteri
886	5	1.5	130	1	ACPS_MYCTU	O53228	mycobacteri
887	5	1.5	130	1	OREX_CANFA	Q9glf6	canis famil
888	5	1.5	130	1	RS9_CLOAB	Q97el3	clostridium
889	5	1.5	130	1	RS9_STRPY	Q99y08	streptococc
890	5	1.5	130	1	Y497_RICPR	Q9zd50	rickettsia
891	5	1.5	130	1	YERA_YEREN	P31490	yersinia en
892	5	1.5	130	1	YERA_YERPE	P31491	yersinia pe
893	5	1.5	131	1	OREX_HUMAN	O43612	homo sapien
894	5	1.5	131	1	OREX_PIG	O77668	sus scrofa
895	5	1.5	131	1	R17A_SCHPO	O42984	schizosacch
896	5	1.5	131	1	RS6E_HALN1	Q9hmj5	halobacteri
897	5	1.5	131	1	RS6E_METJA	P54067	methanococc
898	5	1.5	131	1	VAL2_SLCV	P27445	squash leaf
899	5	1.5	131	1	Y293_AQUAE	O66643	aquifex aeo
900	5	1.5	132	1	MCH_METAL	Q9rpw4	methylomicr
901	5	1.5	132	1	MCH_METRU	Q9rpw2	methylomona
902	5	1.5	132	1	RBFA_PASMU	P57872	pasteurella
903	5	1.5	132	1	RS19_PYRAB	Q9v1t9	pyrococcus
904	5	1.5	132	1	RS19_PYRHO	O59422	pyrococcus
905	5	1.5	132	1	VG14_BPB03	Q37895	bacteriopha
906	5	1.5	132	1	VG25_BPT4	P09425	bacteriopha
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908	5	1.5	133	1	NL21_PARJU	P55958	parietaria
909	5	1.5	133	1	POP8_YEAST	P38208	saccharomyc
910	5	1.5	133	1	TRK4_ECOLI	P17910	escherichia
911	5	1.5	134	1	CY51_ARATH	Q42342	arabidopsis
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913	5	1.5	135	1	FENR_SHIFL	P28901	shigella fl
914	5	1.5	135	1	LEG2_CONMY	Q9yic2	conger myri
915	5	1.5	135	1	VAL2_ICMV	Q08589	indian cass
916	5	1.5	135	1	VE6_PAPVD	P03128	deer papill
917	5	1.5	136	1	MCH_METTO	Q9rpw3	methylococc
918	5	1.5	136	1	NRDI_ECOLI	Q47415	escherichia
919	5	1.5	136	1	NRDI_SALTY	Q56109	salmonella
920	5	1.5	136	1	RK16_MESVI	Q9muu3	mesostigma
921	5	1.5	136	1	RNK_ECOLI	P40679	escherichia
922	5	1.5	136	1	Y14A_MYCPN	P75582	mycoplasma
923	5	1.5	137	1	KDGL_PSEDE	P29945	pseudomonas
924	5	1.5	137	1	NU3M_PODAN	P15580	podospora a
925	5	1.5	137	1	RK16_ODOSI	P49553	odontella s
926	5	1.5	137	1	YSCB_YEREN	Q01243	yersinia en
927	5	1.5	138	1	ARPU_STRTR	O34055	streptococc
928	5	1.5	138	1	NL13_PARJU	Q40905	parietaria
929	5	1.5	138	1	SODM_MYCPA	P53647	mycobacteri
930	5	1.5	139	1	RL16_TREPA	O83226	treponema p
931	5	1.5	139	1	RS16_STRCO	O69879	streptomyce
932	5	1.5	139	1	RS16_STRLI	O86868	streptomyce
933	5	1.5	139	1	Y589_HAEIN	P44020	haemophilus
934	5	1.5	140	1	ADFX_ARATH	O91q81	arabidopsis
935	5	1.5	140	1	PAAI_ECOLI	P76084	escherichia
936	5	1.5	140	1	POP7_YEAST	P38291	saccharomyc
937	5	1.5	140	1	RINA_BPPHA	Q03182	bacteriopha
938	5	1.5	140	1	RS12_CAEEL	P49196	caenorhabdi
939	5	1.5	140	1	VE6_HPV1A	P06929	human papil
940	5	1.5	140	1	VMTG_LAMBD	P03734	bacteriopha
941	5	1.5	140	1	YDAT_ECOLI	P76064	escherichia
942	5	1.5	141	1	HBAD_GEONI	P83124	geochelone
943	5	1.5	141	1	HBAD_PHACA	P10781	phalacrocor
944	5	1.5	141	1	HBAD_PHRHI	P02006	phrynops hi
945	5	1.5	141	1	HBAD_SPHPU	P10062	sphenodon p
946	5	1.5	141	1	HBA_CAMDR	P01974	camelus dro
947	5	1.5	141	1	HBA_LAMGL	P01973	lama glama
948	5	1.5	141	1	HBA_LAMPA	P07426	lama guanic
949	5	1.5	141	1	HBA_LAMVI	P07425	lama vicugn
950	5	1.5	141	1	HBB_DASAK	P56692	dasyatis ak
951	5	1.5	141	1	NFE1_RHIME	Q52993	rhizobium m
952	5	1.5	141	1	VE6_HPV38	Q80907	human papil
953	5	1.5	141	1	YJEB_VIBPA	P40610	vibrio para
954	5	1.5	142	1	A2S1_HUMAN	P53680	homo sapien
955	5	1.5	142	1	A2S1_MOUSE	Q00380	mus musculu
956	5	1.5	142	1	NCB1_YEAST	P40096	saccharomyc
957	5	1.5	142	1	VG46_BPML5	Q05257	mycobacteri
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962	5	1.5	144	1	G20U_BACSU	P80879	bacillus su
963	5	1.5	144	1	GLB3_LAMSP	P15469	lamellibrac
964	5	1.5	144	1	HEX9_ADE12	P03284	human adeno
965	5	1.5	144	1	Y850_HAEIN	P44060	haemophilus
966	5	1.5	144	1	YIG0_YEAST	P40519	saccharomyc
967	5	1.5	145	1	ANF_RANCA	P18909	rana catesb
968	5	1.5	145	1	HBBA_BOSJA	P04346	bos javanic
969	5	1.5	145	1	HBBA_CAPHI	P02077	capra hircu
970	5	1.5	145	1	HBBF_BOVIN	P02081	bos taurus
971	5	1.5	145	1	HBB_ALCAA	P02073	alces alces
972	5	1.5	145	1	HBB_BISBO	P09422	bison bonas
973	5	1.5	145	1	HBB_BOSGF	P02071	bos gaurus
974	5	1.5	145	1	HBB_BOSMU	P02072	bos mutus g
975	5	1.5	145	1	HBB_BOVIN	P02070	bos taurus
976	5	1.5	145	1	HBB_OVIMU	P02076	ovis orient
977	5	1.5	145	1	HBB_TRAST	P04245	tragelaphus
978	5	1.5	145	1	LIRP_LOCMI	P15131	locusta mig
979	5	1.5	145	1	PA20_BUNMU	P00606	bungarus mu
980	5	1.5	145	1	PSAN_HORVU	P31093	hordeum vul
981	5	1.5	145	1	RL11_AQUAE	O67758	aquifex aeo
982	5	1.5	145	1	YAF4_SCHPO	Q09858	schizosacch

983	5	1.5	145	1	YERC_SCHPO	O14095 schizosacch
984	5	1.5	145	1	YTKA_BACSU	P40768 bacillus su
985	5	1.5	146	1	CYM5_RAT	P04166 rattus norv
986	5	1.5	146	1	HBB1_CYGMA	P23017 cygnodraco
987	5	1.5	146	1	HBB1_MOUSE	P02088 mus musculu
988	5	1.5	146	1	HBB1_PAGBO	O93348 pagothenia
989	5	1.5	146	1	HBB2_MOUSE	P02089 mus musculu
990	5	1.5	146	1	HBB2_PANLE	P18988 panthera le
991	5	1.5	146	1	HBB2_TRENE	O93349 trematomus
992	5	1.5	146	1	HBB_AEGMO	P07418 aegypius mo
993	5	1.5	146	1	HBB_AILFU	P18982 ailurus ful
994	5	1.5	146	1	HBB_AILME	P18983 ailuropoda
995	5	1.5	146	1	HBB_ANAPL	P02114 anas platyr
996	5	1.5	146	1	HBB_ANAPP	P02115 anas platyr
997	5	1.5	146	1	HBB_ANSAN	P02117 anser anser
998	5	1.5	146	1	HBB_ANSIN	P02118 anser indic
999	5	1.5	146	1	HBB_ANSSE	P02120 anseranas s
1000	5	1.5	146	1	HBB_AOTTR	P02035 aotus trivi

ALIGNMENTS

```
RESULT   1
ZIPA_ECOLI
ID   ZIPA_ECOLI     STANDARD;      PRT;   328 AA.
AC   P77173;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cell division protein zipA.
GN   ZIPA OR B2412.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PB103;
RX   MEDLINE=97160838; PubMed=9008158;
RA   Hale C.A., de Boer P.A.J.;
RT   "Direct binding of FtsZ to ZipA, an essential component of the septal
RT   ring structure that mediates cell division in E. coli.";
RL   Cell 88:175-185(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97349980; PubMed=9205837;
RA   Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA   Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA   Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA   Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA   Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA   Yamagata S., Horiuchi T.;
RT   "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT   -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT   analysis of its sequence features.";
RL   DNA Res. 4:91-113(1997).
RN   [4]
RP   STRUCTURE BY NMR OF 185-328.
RX   MEDLINE=20384201; PubMed=10924108;
RA   Moy F.J., Glasfeld E., Mosyak L., Powers R.;
RT   "Solution structure of ZipA, a crucial component of Escherichia coli
RT   cell division.";
RL   Biochemistry 39:9146-9156(2000).
CC   -!- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC       Probable receptor for the septal ring structure, may anchor it
CC       to the inner-membrane.
CC   -!- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U74650; AAB42061.1; -.
DR   EMBL; AE000329; AAC75465.1; -.
DR   EMBL; D90870; BAA16284.1; -.
DR   PDB; 1F7X; 28-JUN-01.
DR   PDB; 1F7W; 28-JUN-01.
DR   EcoGene; EG14169; zipA.
KW   Cell division; Septation; Transmembrane; Inner membrane; 3D-structure;
KW   Complete proteome.
FT   DOMAIN        1      6       PERIPLASMIC (POTENTIAL).
FT   TRANSMEM      7     27       POTENTIAL.
FT   DOMAIN       28    328       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    211    211       A -> L (IN REF. 2).
SQ   SEQUENCE   328 AA;  36433 MW;  020F1197153F9BAD CRC64;


  Query Match             100.0%;  Score 328;  DB 1;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  328;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60
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Db       1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYDEDVEDD 60

Qy      61 EGVGEVRVHRVNHAPANAQEHEAARPSPQHQYQPPYASAQPRQPVQQPPEAQVPPQHAPH 120
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Qy     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180
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Db     121 PAQPVQQPAYQPQPEQPLQQPVSPQVAPAPQPVHSAPQPAQQAFQPAEPVAAPQPEPVAE 180

Qy     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGEALLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240
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Db     181 PAPVMDKPKRKEAVIIMNVAAHHGSELNGEALLNSIQQAGFIFGDMNIYHRHLSPDGSGP 240

Qy     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQNFKLMLQSAQHIADEVGGVV 300

Qy     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328
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Db     301 LDDQRRMMTPQKLREYQDIIREVKDANA 328


RESULT   2
ZIPA_SALTY
ID   ZIPA_SALTY     STANDARD;      PRT;   328 AA.
AC   P55894;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cell division protein zipA.
GN   ZIPA OR STM2428 OR STY2664.
OS   Salmonella typhimurium, and
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
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OX   NCBI_TaxID=602, 601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
RN   [2]
RP   SEQUENCE OF 1-32 FROM N.A.
RC   SPECIES=S.typhimurium; STRAIN=LT2;
RX   MEDLINE=88257033; PubMed=3290198;
RA   Byrne C.R., Monroe R.S., Ward K.A., Kredich N.M.;
RT   "DNA sequences of the cysK regions of Salmonella typhimurium and
RT   Escherichia coli and linkage of the cysK regions to ptsH.";
RL   J. Bacteriol. 170:3150-3157(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.typhi; STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
CC   -!- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC       Probable receptor for the septal ring structure, may anchor it
CC       to the inner-membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE008809; AAL21322.1; -.
DR   EMBL; M21450; -; NOT_ANNOTATED_CDS.
DR   EMBL; AL627274; CAD07660.1; -.
DR   StyGene; SG10748; zipA.
KW   Cell division; Septation; Transmembrane; Inner membrane;
KW   Complete proteome.
FT   DOMAIN        1      6       PERIPLASMIC (POTENTIAL).
FT   TRANSMEM      7     27       POTENTIAL.
FT   DOMAIN       28    328       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   328 AA;  36318 MW;  B8A44F708AF35F13 CRC64;


  Query Match             16.5%;  Score 54;  DB 1;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-47;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYD 54
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSKRDDDSYD 54


RESULT   3
ZIPA_YERPE
ID   ZIPA_YERPE     STANDARD;      PRT;   328 AA.
AC   P58492;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cell division protein zipA homolog.
GN   ZIPA OR YPO2990.
OS   Yersinia pestis.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Yersinia.
OX   NCBI_TaxID=632;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CO-92 / Biovar Orientalis;
RX   MEDLINE=21470413; PubMed=11586360;
RA   Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA   Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
RA   Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA   Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA   Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA   Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA   Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT   "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL   Nature 413:523-527(2001).
CC   -!- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC       Probable receptor for the septal ring structure, may anchor it
CC       to the inner-membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ414154; CAC92234.1; -.
KW   Cell division; Septation; Transmembrane; Inner membrane;
KW   Complete proteome.
FT   DOMAIN        1      4       PERIPLASMIC (POTENTIAL).
FT   TRANSMEM      5     25       POTENTIAL.
FT   DOMAIN       26    328       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   328 AA;  36098 MW;  EA04B89084649044 CRC64;


  Query Match              3.4%;  Score 11;  DB 1;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 0.0021;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    242 LFSLANMVKPG 252
          ||||||||||||
Db    239 LFSLANMVKPG 249


RESULT   4
MBR1_YEAST
ID   MBR1_YEAST     STANDARD;      PRT;   339 AA.
AC   P23493;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   MBR1 protein.
GN   MBR1 OR YKL093W OR YKL440.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=R100;
RX   MEDLINE=94268503; PubMed=8208248;
RA   Daignan-Fornier B., Nguyen C.C., Reisdorf P., Lemeignan B.,
RA   Bolotin-Fukuhara M.;
RT   "MBR1 and MBR3, two related yeast genes that can suppress the growth
RT   defect of hap2, hap3 and hap4 mutants.";
RL   Mol. Gen. Genet. 243:575-583(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RX   MEDLINE=94078677; PubMed=8256524;
RA   Pallier C., Valens M., Puzos V., Fukuhara H., Cheret G., Sor F.,
RA   Bolotin-Fukuhara M.;
RT   "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI
RT   physically localizes the MRB1 gene and reveals eight new open reading
RT   frames, including a homologue of the KIN1/KIN2 and SNF1 protein
RT   kinases.";
RL   Yeast 9:1149-1155(1993).
RN   [3]
RP   SEQUENCE OF 169-339 FROM N.A.
RX   MEDLINE=94262329; PubMed=8203166;
RA   James C.M., Gent M.E., Oliver S.G.;
RT   "Sequence analysis of a 3.5 Kb EcoRI fragment from the left arm of
RT   Saccharomyces cerevisiae chromosome XI reveals the location of the
RT   MBR1 gene and a sequence related to a GTPase-activating protein.";
RL   Yeast 10:257-264(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=92215853; PubMed=1725263;
RA   Valens M., Rinaldi T., Daignan-Fornier B., Bolotin-Fukuhara M.;
RT   "Identification of nuclear genes which participate to mitochondrial
RT   translation in Saccharomyces cerevisiae.";
RL   Biochimie 73:1525-1532(1991).
CC   -!- FUNCTION: PARTICIPATES IN MITOCHONDRIAL BIOGENESIS.
CC   -!- SIMILARITY: STRONG, TO MBR3.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63309; AAA88725.1; -.
DR   EMBL; X71133; CAA50464.1; -.
DR   EMBL; X75561; CAA53240.1; -.
DR   EMBL; Z28093; CAA81931.1; -.
DR   PIR; S37920; S37920.
DR   SGD; S0001576; MBR1.
KW   Mitochondrion.
FT   CONFLICT     88     88       A -> G (IN REF. 1).
FT   CONFLICT    168    168       G -> R (IN REF. 1).
FT   CONFLICT    206    206       S -> T (IN REF. 1).
FT   CONFLICT    245    245       G -> E (IN REF. 1).
SQ   SEQUENCE   339 AA;  36934 MW;  A38E7EA7049754A0 CRC64;


  Query Match             2.4%;  Score 8;  DB 1;  Length 339;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     100 QPRQPVQQ 107
           ||||||||
Db     305 QPRQPVQQ 312


RESULT   5
YHHS_ECOLI
ID   YHHS_ECOLI     STANDARD;      PRT;   419 AA.
AC   P37621;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Hypothetical protein yhhS.
GN   YHHS OR B3473.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=94316500; PubMed=8041620;
RA   Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT   "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT   region from 76.0 to 81.5 minutes.";
RL   Nucleic Acids Res. 22:2576-2586(1994).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U00039; CAB34656.1; -.
DR   EMBL; AE000423; AAC76498.1; -.
DR   EcoGene; EG12219; yhhS.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   419 AA;  43783 MW;  2260CA0E17438CFF CRC64;


  Query Match             2.4%;  Score 8;  DB 1;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEPA 182
           ||||||||
Db      16 PEPVAEPA 23


RESULT   6
BCHB_CHLAU
ID   BCHB_CHLAU     STANDARD;      PRT;   541 AA.
AC   Q9F6X5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Light-independent protochlorophyllide reductase subunit B
DE   (EC 1.18.-.-) (LI-POR subunit B) (DPOR subunit B).
GN   BCHB.
OS   Chloroflexus aurantiacus.
OC   Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
OC   Chloroflexaceae; Chloroflexus.
OX   NCBI_TaxID=1108;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20433268; PubMed=10976061;
RA   Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
RT   "Molecular evidence for the early evolution of photosynthesis.";
RL   Science 289:1724-1730(2000).
CC   -!- FUNCTION: Uses Mg-ATP and reduced ferredoxin to reduce ring D of
CC       protochlorophyllide (Pchlide) to form chlorophyllide a (Chlide)
CC       (By similarity). This reaction is light-independent.
CC   -!- PATHWAY: Light-independent bacteriochlorophyll biosynthesis.
CC   -!- SUBUNIT: Protochlorophyllide reductase is thought to be composed
CC       of three subunits; bchL, bchN and bchB. Could form a
CC       heterotetramer of two bchB and two bchN subunits.
CC   -!- SIMILARITY: BELONGS TO THE CHLB / BCHB / BCHZ FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF288460; AAG15210.1; -.
DR   InterPro; IPR000510; Oxidored_nitrognse_1.
DR   Pfam; PF00148; oxidored_nitro; 2.
KW   Oxidoreductase; Photosynthesis; Bacteriochlorophyll biosynthesis.
SQ   SEQUENCE   541 AA;  59181 MW;  0F3060E48358A5F7 CRC64;


  Query Match             2.4%;  Score 8;  DB 1;  Length 541;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     177 PVAEPAPV 184
           ||||||||
Db     445 PVAEPAPV 452


RESULT   7
ALU8_HUMAN
ID   ALU8_HUMAN     STANDARD;      PRT;   591 AA.
AC   P39195;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alu subfamily SX sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC       POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC       ACID SEQUENCES.
CC   -!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC       PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC       ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
CC       ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS: HOWEVER,
CC       CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
CC       LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC       ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC       GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC       CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC       OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC       CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC       DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC       THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC       BEING REPORTED.
CC   -!- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC       WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC       PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC       CODING NUCLEOTIDE SEQUENCE.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U14574; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN        1     96       FRAME-1.
FT   DOMAIN      100    195       FRAME-2.
FT   DOMAIN      199    294       FRAME-3.
FT   DOMAIN      298    393       FRAME-4.
FT   DOMAIN      397    492       FRAME-5.
FT   DOMAIN      496    591       FRAME-6.
SQ   SEQUENCE   591 AA;  64395 MW;  AC8154AD8A6BB280 CRC64;


  Query Match             2.4%;  Score 8;  DB 1;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     244 SLANMVKP 251
           ||||||||
Db     227 SLANMVKP 234


RESULT   8
ALU7_HUMAN
ID   ALU7_HUMAN     STANDARD;      PRT;   593 AA.
AC   P39194;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alu subfamily SQ sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
```

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RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC       POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC       ACID SEQUENCES.
CC   -!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC       PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC       ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
CC       ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC       CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
CC       LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC       ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC       GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC       CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC       OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC       CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC       DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC       THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC       BEING REPORTED.
CC   -!- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC       WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC       PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC       CODING NUCLEOTIDE SEQUENCE.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U14573; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN        1     97       FRAME-1.
FT   DOMAIN      101    196       FRAME-2.
FT   DOMAIN      200    295       FRAME-3.
FT   DOMAIN      299    395       FRAME-4.
FT   DOMAIN      399    494       FRAME-5.
FT   DOMAIN      498    593       FRAME-6.
SQ   SEQUENCE   593 AA;  64417 MW;  54A4F50F33A6089F CRC64;


  Query Match             2.4%;  Score 8;  DB 1;  Length 593;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     244 SLANMVKP 251
           ||||||||
Db     228 SLANMVKP 235


RESULT   9
LHA3_ECTHA
ID   LHA3_ECTHA     STANDARD;      PRT;    49 AA.
AC   P80107;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Light-harvesting protein B800/850/890, alpha-3 chain (EHA-alpha-3)
DE   (Antenna pigment protein, alpha-3 chain) (Fragment).
OS   Ectothiorhodospira halophila.
OC   Bacteria; Proteobacteria; gamma subdivision; Ectothiorhodospiraceae;
OC   Halorhodospira.
OX   NCBI_TaxID=1053;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=DSM 244;
RX   MEDLINE=92249336; PubMed=1577009;
RA   Wagner-Huber R., Brunisholz R.A., Bissig I., Frank G., Suter F.,
RA   Zuber H.;
RT   "The primary structure of the antenna polypeptides of
RT   Ectothiorhodospira halochloris and Ectothiorhodospira halophila. Four
RT   core-type antenna polypeptides in E. halochloris and E. halophila.";
RL   Eur. J. Biochem. 205:917-925(1992).
CC   -!- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH
CC       TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
CC   -!- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA
CC       CHAINS, BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED
CC       MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
CC       REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
CC       ADDITIONAL COMPONENTS.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
DR   PIR; S23290; S23290.
DR   HSSP; P26789; 1KZU.
DR   InterPro; IPR002361; Antenna_comp_alpha.
DR   InterPro; IPR000066; LHC.
DR   Pfam; PF00556; LHC; 1.
DR   PROSITE; PS00968; ANTENNA_COMP_ALPHA; 1.
KW   Antenna complex; Light-harvesting polypeptide; Transmembrane;
KW   Magnesium; Bacteriochlorophyll; Inner membrane.
FT   DOMAIN        1     14       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     15     35       POTENTIAL.
FT   DOMAIN       36    >49       PERIPLASMIC (POTENTIAL).
FT   METAL        31     31       AXIAL LIGAND TO THE BACTERIOCHLOROPHYLL
FT                                MAGNESIUM (POTENTIAL).
FT   NON_TER      49     49
SQ   SEQUENCE   49 AA;  5479 MW;  753BFC2EC2014419 CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      18 IALLVHG 24
           |||||||
Db      26 IALLVHG 32


RESULT  10
RL17_LEPIN
ID   RL17_LEPIN     STANDARD;      PRT;   178 AA.
AC   Q9XD08;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   50S ribosomal protein L17.
GN   RPLQ.
OS   Leptospira interrogans.
OC   Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
OX   NCBI_TaxID=173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROVAR LAI;
RX   MEDLINE=20088835; PubMed=10620683;
RA   Zuerner R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.;
RT   "Characterization of the Leptospira interrogans S10-spc-alpha
RT   operon.";
RL   FEMS Microbiol. Lett. 182:303-308(2000).
CC   -!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF115283; AAD40611.1; -.
DR   InterPro; IPR000456; Ribosomal_L17.
DR   Pfam; PF01196; Ribosomal_L17; 1.
DR   ProDom; PD004277; Ribosomal_L17; 1.
DR   PROSITE; PS01167; RIBOSOMAL_L17; 1.
KW   Ribosomal protein.
SQ   SEQUENCE   178 AA;  20902 MW;  FB06DCE4950B5740 CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      27 TSRKERS 33
           |||||||
Db     125 TSRKERS 131


RESULT  11
RS3A_HALN1
ID   RS3A_HALN1     STANDARD;      PRT;   206 AA.
AC   Q9HRA5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   30S ribosomal protein S3Ae.
GN   RPS3AE OR RPS3E OR VNG0787G.
OS   Halobacterium sp. (strain NRC-1).
OC   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC   Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC   -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE005021; AAG19253.1; -.
DR   InterPro; IPR001593; Ribosomal_S3AE.
DR   Pfam; PF01015; Ribosomal_S3Ae; 1.
DR   ProDom; PD003035; Ribosomal_S3AE; 1.
DR   PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE_NEG.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE   206 AA;  23362 MW;  8E5033F7AA28DD60 CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     210 EALLNSI 216
           |||||||
Db     151 EALLNSI 157


RESULT  12
GRPS_MYXXA
ID   GRPS_MYXXA     STANDARD;      PRT;   255 AA.
AC   P95333;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   GrpS protein.
GN   GRPS.
OS   Myxococcus xanthus.
OC   Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC   Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX   NCBI_TaxID=34;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DK1622;
RA   Weimer R., Hartzell P.L., Youderian P.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: POTENTIAL CHAPERONE FOR OTHER PROTEINS INVOLVED IN
CC       SOCIAL MOTILITY.
CC   -!- SIMILARITY: BELONGS TO THE GRPE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U83800; AAC64204.1; -.
DR   HSSP; P09372; 1DKG.
DR   InterPro; IPR000740; GrpE.
DR   Pfam; PF01025; GrpE; 1.
DR   PRINTS; PR00773; GRPEPROTEIN.
DR   PROSITE; PS01071; GRPE; 1.
KW   Chaperone.
SQ   SEQUENCE   255 AA;  27390 MW;  7A41F433563D10C0 CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     166 PAEPVAA 172
           |||||||
Db     216 PAEPVAA 222


RESULT  13
TRT1_HUMAN
ID   TRT1_HUMAN     STANDARD;      PRT;   277 AA.
AC   P13805;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Troponin T, slow skeletal muscle isoforms (Slow skeletal muscle
DE   troponin T).
GN   TNNT1 OR TNT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88058976; PubMed=2824479;
RA   Gahlmann R., Troutt A.B., Wade R.P., Gunning P., Kedes L.;
RT   "Alternative splicing generates variants in important functional
RT   domains of human slow skeletal troponin T.";
```

```
RL   J. Biol. Chem. 262:16122-16126(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=94183266; PubMed=8135831;
RA   Samson F., Mesnard L., Mihovilovic M., Potter T.G., Mercadier J.-J.,
RA   Roses A.D., Gilbert J.R.;
RT   "A new human slow skeletal troponin T (TnTs) mRNA isoform derived
RT   from alternative splicing of a single gene.";
RL   Biochem. Biophys. Res. Commun. 199:841-847(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99208666; PubMed=10191089;
RA   Barton P.J.R., Cullen M.E., Townsend P.J., Brand N.J., Mullen A.J.,
RA   Norman D.A.M., Bhavsar P.K., Yacoub M.H.;
RT   "Close physical linkage of human troponin genes: organization,
RT   sequence, and expression of the locus encoding cardiac troponin I and
RT   slow skeletal troponin T.";
RL   Genomics 57:102-109(1999).
CC   -!- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
CC       TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
CC       CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
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CC   ---------------------------------------------------------------------
DR   EMBL; M19309; AAA61204.1; -.
DR   EMBL; M19308; AAA61205.1; -.
DR   EMBL; S69208; AAB30272.1; -.
DR   EMBL; S69209; AAB30273.1; -.
DR   EMBL; AJ011712; CAA09751.1; -.
DR   EMBL; AJ011713; CAA09751.1; JOINED.
DR   EMBL; AJ011712; CAA09752.1; -.
DR   EMBL; AJ011713; CAA09752.1; JOINED.
DR   PIR; A29783; A29783.
DR   MIM; 191041; -.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Muscle protein; Phosphorylation; Alternative splicing;
KW   Multigene family.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       PHOSPHORYLATION (BY CK2)
FT                                (BY SIMILARITY).
FT   VARSPLIC     24     34       MISSING (IN ISOFORM 2).
FT   VARSPLIC    204    219       MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT   CONFLICT     19     19       E -> D (IN REF. 1).
SQ   SEQUENCE   277 AA;  32817 MW;  4064FC1F359E663D CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 277;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     175 PEPVAEP 181
           |||||||
Db      28 PEPVAEP 34


RESULT  14
ALF_MYCGE
ID   ALF_MYCGE      STANDARD;      PRT;   288 AA.
AC   P47269;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fructose-bisphosphate aldolase (EC 4.1.2.13).
GN   FBA OR TSR OR MG023.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
CC   -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC       phosphate + D-glyceraldehyde 3-phosphate.
CC   -!- COFACTOR: ZINC (BY SIMILARITY).
CC   -!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U39681; AAC71239.1; -.
DR   HSSP; P11604; 1ZEN.
DR   TIGR; MG023; -.
DR   InterPro; IPR000771; F_bP_aldolase.
DR   Pfam; PF01116; F_bP_aldolase; 1.
DR   PROSITE; PS00602; ALDOLASE_CLASS_II_1; 1.
DR   PROSITE; PS00806; ALDOLASE_CLASS_II_2; 1.
KW   Lyase; Glycolysis; Zinc; Complete proteome.
FT   METAL        82     82       ZINC (BY SIMILARITY).
FT   METAL        85     85       ZINC (BY SIMILARITY).
SQ   SEQUENCE   288 AA;  31310 MW;  BD09F4683DD6A32F CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 288;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     281 NFKLMLQ 287
           |||||||
Db       4 NFKLMLQ 10


RESULT  15
ZIPA_PSEAE
ID   ZIPA_PSEAE     STANDARD;      PRT;   289 AA.
AC   Q9I3I5;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cell division protein zipA homolog.
GN   ZIPA OR PA1528.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
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RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
CC   -!- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC       Probable receptor for the septal ring structure, may anchor it
CC       to the inner-membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE004581; AAG04917.1; -.
DR   HSSP; P77173; 1F7X.
KW   Cell division; Septation; Transmembrane; Inner membrane;
KW   Complete proteome.
FT   DOMAIN        1      6       PERIPLASMIC (POTENTIAL).
FT   TRANSMEM      7     27       POTENTIAL.
FT   DOMAIN       28    289       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   289 AA;  32236 MW;  720D6FED832B329C CRC64;


  Query Match             2.1%;  Score 7;  DB 1;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     249 VKPGTFD 255
           |||||||
Db     205 VKPGTFD 211


Search completed: September 25, 2002, 09:57:04
Job time: 248 sec
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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:52:41 ; Search time 28.68 Seconds
(without alignments)
1978.464 Million cell updates/sec

Title: US-09-184-826-2
Perfect score: 328
Sequence: 1 MMQDLRLILIIVGAIAIIAL.....TPQKLREYQDIIREVKDANA 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	2.7	137	5	Q20468	Q20468 caenorhabdi
2	9	2.7	522	15	Q9WLL1	Q9wll1 mus dunni e
3	9	2.7	622	15	O89814	O89814 mus dunni e
4	8	2.4	130	17	Q9HNM8	Q9hnm8 halobacteri
5	8	2.4	210	5	Q9XYB2	Q9xyb2 plasmodium
6	8	2.4	222	2	Q9ADC6	Q9adc6 streptomyce
7	8	2.4	234	16	Q92LX9	Q92lx9 rhizobium m
8	8	2.4	400	5	Q95RV8	Q95rv8 drosophila
9	8	2.4	431	2	Q9S333	Q9s333 prochloroco
10	8	2.4	441	13	O57311	O57311 xenopus lae
11	8	2.4	457	10	Q9SSF3	Q9ssf3 arabidopsis
12	8	2.4	512	16	Q9CGA7	Q9cga7 lactococcus
13	8	2.4	620	5	Q9VKL0	Q9vkl0 drosophila
14	8	2.4	1476	5	Q9Y0W1	Q9y0w1 drosophila
15	8	2.4	1476	5	Q9V9T4	Q9v9t4 drosophila
16	8	2.4	1476	5	Q9NG24	Q9ng24 drosophila
17	8	2.4	2485	5	O96134	O96134 plasmodium
18	7	2.1	72	15	P90474	P90474 walleye der
19	7	2.1	72	15	P89225	P89225 walleye der
20	7	2.1	72	15	P89226	P89226 walleye der
21	7	2.1	72	15	P89227	P89227 walleye der
22	7	2.1	72	15	P89229	P89229 walleye der
23	7	2.1	72	15	P89230	P89230 walleye der
24	7	2.1	72	15	P89234	P89234 walleye der
25	7	2.1	81	5	Q9W5Q0	Q9w5q0 drosophila
26	7	2.1	82	10	Q9SJD2	Q9sjd2 arabidopsis
27	7	2.1	85	15	Q99DB2	Q99db2 human immun
28	7	2.1	85	15	Q99DA7	Q99da7 human immun
29	7	2.1	87	4	Q9UI59	Q9ui59 homo sapien
30	7	2.1	93	15	O41565	O41565 human immun
31	7	2.1	116	12	Q9YJQ1	Q9yjq1 african cas
32	7	2.1	116	12	Q9IN46	Q9in46 south afric
33	7	2.1	120	2	Q93PB7	Q93pb7 microscilla
34	7	2.1	121	2	Q9L5G7	Q9l5g7 salmonella
35	7	2.1	137	15	Q9DRS8	Q9drs8 human immun
36	7	2.1	144	10	Q9FME9	Q9fme9 arabidopsis
37	7	2.1	148	11	O35427	O35427 mus musculu
38	7	2.1	152	15	Q9DRS6	Q9drs6 human immun
39	7	2.1	162	2	Q9KYB6	Q9kyb6 streptomyce
40	7	2.1	176	5	Q23186	Q23186 caenorhabdi
41	7	2.1	184	15	Q9DRS7	Q9drs7 human immun
42	7	2.1	186	5	O16567	O16567 caenorhabdi
43	7	2.1	187	2	Q9JRL5	Q9jrl5 xanthomonas
44	7	2.1	199	4	Q96AH8	Q96ah8 homo sapien
45	7	2.1	202	5	Q18903	Q18903 caenorhabdi
46	7	2.1	206	15	Q9DRS9	Q9drs9 human immun
47	7	2.1	206	15	Q9DRS4	Q9drs4 human immun
48	7	2.1	212	16	Q9PJS8	Q9pjs8 chlamydia m
49	7	2.1	213	16	O84471	O84471 chlamydia t
50	7	2.1	223	5	Q9VLM7	Q9vlm7 drosophila
51	7	2.1	238	9	Q9ZX83	Q9zx83 bacteriopha
52	7	2.1	246	4	Q9BTW8	Q9btw8 homo sapien
53	7	2.1	246	16	O51211	O51211 borrelia bu
54	7	2.1	250	10	Q39956	Q39956 helianthus
55	7	2.1	252	4	Q9HAI3	Q9hai3 homo sapien
56	7	2.1	252	4	Q96A62	Q96a62 homo sapien
57	7	2.1	271	10	Q9FWB9	Q9fwb9 oryza sativ
58	7	2.1	272	16	Q9I1L8	Q9i118 pseudomonas
59	7	2.1	275	12	O56822	O56822 human cytom
60	7	2.1	280	2	Q9ZF37	Q9zf37 lactobacill
61	7	2.1	285	16	Q97NH0	Q97nh0 streptococc
62	7	2.1	288	5	Q9XYV5	Q9xyv5 toxocara ca
63	7	2.1	289	16	Q9I3I5	Q9i3i5 pseudomonas
64	7	2.1	290	2	Q9RBQ3	Q9rbq3 xanthomonas
65	7	2.1	290	2	Q9RBQ2	Q9rbq2 xanthomonas
66	7	2.1	290	2	Q9F238	Q9f238 xanthomonas
67	7	2.1	290	2	O51899	O51899 xanthomonas
68	7	2.1	290	10	Q9S7K0	Q9s7k0 oryza sativ
69	7	2.1	290	16	Q9KAU2	Q9kau2 bacillus ha
70	7	2.1	291	16	Q9KTD2	Q9ktd2 vibrio chol
71	7	2.1	295	2	O32850	O32850 mycobacteri
72	7	2.1	309	3	Q9P6R1	Q9p6r1 schizosacch
73	7	2.1	312	16	Q9KS96	Q9ks96 vibrio chol
74	7	2.1	330	4	Q9Y292	Q9y292 homo sapien
75	7	2.1	330	4	Q96AT8	Q96at8 homo sapien
76	7	2.1	340	17	Q9YCJ2	Q9ycj2 aeropyrum p
77	7	2.1	343	10	Q9AUW7	Q9auw7 oryza sativ
78	7	2.1	346	16	Q98FL9	Q98fl9 rhizobium l
79	7	2.1	355	5	Q9NGQ7	Q9ngq7 ostrinia nu
80	7	2.1	356	12	Q88524	Q88524 turkey herp
81	7	2.1	356	16	Q9PA12	Q9pa12 xylella fas
82	7	2.1	358	16	Q9JY93	Q9jy93 neisseria m
83	7	2.1	358	16	Q9JT75	Q9jt75 neisseria m
84	7	2.1	361	5	Q9W1P2	Q9w1p2 drosophila
85	7	2.1	364	11	O70509	O70509 rattus norv
86	7	2.1	365	11	Q99J14	Q99j14 mus musculu
87	7	2.1	372	3	Q9UUJ0	Q9uuj0 schizosacch
88	7	2.1	380	16	Q9CIV1	Q9civ1 lactococcus
89	7	2.1	396	17	Q9V2R1	Q9v2r1 pyrococcus

90	7	2.1	404	16	Q99W82	Q99w82 staphylococ
91	7	2.1	412	2	Q52939	Q52939 rhizobium m
92	7	2.1	422	2	Q9RJ50	Q9rj50 streptomyce
93	7	2.1	440	12	Q9Q6P7	Q9q6p7 grapevine l
94	7	2.1	445	16	Q9CP12	Q9cp12 pasteurella
95	7	2.1	455	5	O61747	O61747 caenorhabdi
96	7	2.1	461	8	Q33748	Q33748 arbacia lix
97	7	2.1	467	4	Q9NXI1	Q9nxi1 homo sapien
98	7	2.1	485	5	O45265	O45265 caenorhabdi
99	7	2.1	489	16	Q984Y5	Q984y5 rhizobium l
100	7	2.1	502	16	Q9RS41	Q9rs41 deinococcus
101	7	2.1	523	17	Q970N4	Q970n4 sulfolobus
102	7	2.1	525	2	Q59813	Q59813 streptomyce
103	7	2.1	540	10	Q9FJ30	Q9fj30 arabidopsis
104	7	2.1	548	16	O06404	O06404 mycobacteri
105	7	2.1	551	2	Q9KZS2	Q9kzs2 streptomyce
106	7	2.1	562	3	Q9UVB9	Q9uvb9 pichia cife
107	7	2.1	562	5	O02054	O02054 caenorhabdi
108	7	2.1	579	11	Q9QZA3	Q9qza3 mus musculu
109	7	2.1	586	4	Q9UQR9	Q9uqr9 homo sapien
110	7	2.1	609	10	Q9XGA4	Q9xga4 spermatozop
111	7	2.1	609	16	Q9A6T7	Q9a6t7 caulobacter
112	7	2.1	614	10	Q94FV3	Q94fv3 lycopersico
113	7	2.1	615	5	P91573	P91573 caenorhabdi
114	7	2.1	638	16	Q988L4	Q98814 rhizobium l
115	7	2.1	644	5	Q9N4W3	Q9n4w3 caenorhabdi
116	7	2.1	654	10	Q9LIW2	Q9liw2 oryza sativ
117	7	2.1	677	12	Q91DD8	Q91dd8 ebola virus
118	7	2.1	693	16	Q9A537	Q9a537 caulobacter
119	7	2.1	696	5	Q9VL53	Q9vl53 drosophila
120	7	2.1	699	11	Q99K46	Q99k46 mus musculu
121	7	2.1	707	10	Q9FGU4	.Q9fgu4 arabidopsis
122	7	2.1	711	4	O60899	O60899 homo sapien
123	7	2.1	717	4	Q9UHZ9	Q9uhz9 homo sapien
124	7	2.1	717	4	Q9H307	Q9h307 homo sapien
125	7	2.1	725	11	O35691	O35691 mus musculu
126	7	2.1	731	4	O60433	O60433 homo sapien
127	7	2.1	736	10	Q9ZWB9	Q9zwb9 arabidopsis
128	7	2.1	743	4	Q99738	Q99738 homo sapien
129	7	2.1	744	5	Q9GPJ1	Q9gpj1 drosophila
130	7	2.1	745	17	Q9Y9L3	Q9y913 aeropyrum p
131	7	2.1	759	4	Q9BWP7	Q9bwp7 homo sapien
132	7	2.1	762	2	O87714	O87714 caulobacter
133	7	2.1	762	16	Q9AB02	Q9ab02 caulobacter
134	7	2.1	780	11	Q9QYX8	Q9qyx8 mus musculu
135	7	2.1	780	11	O08779	O08779 rattus norv
136	7	2.1	810	5	Q9U4G9	Q9u4g9 drosophila
137	7	2.1	812	16	Q98IK0	Q98ik0 rhizobium l
138	7	2.1	815	4	O43273	O43273 homo sapien
139	7	2.1	824	4	Q9BZY2	Q9bzy2 homo sapien
140	7	2.1	829	4	Q9BZX7	Q9bzx7 homo sapien
141	7	2.1	848	10	Q9LS51	Q9ls51 arabidopsis
142	7	2.1	848	16	Q98MT4	Q98mt4 rhizobium l
143	7	2.1	854	4	Q9BZY1	Q9bzy1 homo sapien
144	7	2.1	874	2	O54159	O54159 streptomyce
145	7	2.1	879	2	Q9FBJ2	Q9fbj2 streptomyce
146	7	2.1	880	5	O17338	O17338 caenorhabdi
147	7	2.1	885	5	Q9TXR9	Q9txr9 caenorhabdi
148	7	2.1	899	16	Q92Z73	Q92z73 rhizobium m
149	7	2.1	911	3	Q96UB8	Q96ub8 neurospora
150	7	2.1	930	5	O17339	O17339 caenorhabdi
151	7	2.1	980	4	Q9NS55	Q9ns55 homo sapien
152	7	2.1	1045	4	Q9NS56	Q9ns56 homo sapien
153	7	2.1	1045	4	Q9UNR9	Q9unr9 homo sapien
154	7	2.1	1049	5	Q9VJ14	Q9vj14 drosophila
155	7	2.1	1123	5	Q9W4P6	Q9w4p6 drosophila
156	7	2.1	1212	2	Q9L1C8	Q9l1c8 streptomyce
157	7	2.1	1233	5	Q9VGY6	Q9vgy6 drosophila
158	7	2.1	1306	11	Q9JK31	Q9jk31 mus musculu
159	7	2.1	1362	4	Q96PD3	Q96pd3 homo sapien
160	7	2.1	1420	3	O13736	O13736 schizosacch
161	7	2.1	1448	16	Q9HYW9	Q9hyw9 pseudomonas
162	7	2.1	1586	13	Q9DFB7	Q9dfb7 gallus gall
163	7	2.1	2274	5	Q9VYU0	Q9vyu0 drosophila
164	7	2.1	2777	10	Q9C7S8	Q9c7s8 arabidopsis
165	7	2.1	2977	5	Q9VAP9	Q9vap9 drosophila
166	7	2.1	4290	2	Q9WXC0	Q9wxc0 micromonosp
167	7	2.1	5476	5	Q9NJ17	Q9nj17 drosophila
168	7	2.1	5533	5	Q9U6C3	Q9u6c3 drosophila
169	7	2.1	5533	5	Q9VPL2	Q9vpl2 drosophila
170	7	2.1	5554	5	Q9NHN1	Q9nhn1 drosophila
171	7	2.1	5560	5	Q9VPL1	Q9vpl1 drosophila
172	6	1.8	18	12	Q9IBM7	Q9ibm7 autographa
173	6	1.8	24	13	Q9PRS8	Q9prs8 gallus gall
174	6	1.8	26	10	Q9S907	Q9s907 avena sativ
175	6	1.8	38	10	Q9ARK2	Q9ark2 paeonia mai
176	6	1.8	39	9	O64160	O64160 bacteriopha
177	6	1.8	39	10	Q9ARK3	Q9ark3 paeonia obo
178	6	1.8	39	16	O31888	O31888 bacillus su
179	6	1.8	40	10	Q9ARJ7	Q9arj7 paeonia del
180	6	1.8	40	10	Q9ARJ5	Q9arj5 paeonia suf
181	6	1.8	40	10	Q9ARJ0	Q9arj0 paeonia cal
182	6	1.8	41	10	Q9ATP9	Q9atp9 paeonia vei
183	6	1.8	41	10	Q9ARK6	Q9ark6 paeonia lac
184	6	1.8	41	10	Q9ARK4	Q9ark4 paeonia ten
185	6	1.8	41	10	Q9ARK0	Q9ark0 paeonia lut
186	6	1.8	42	10	Q9ARJ1	Q9arj1 paeonia sze
187	6	1.8	43	10	Q9ARK8	Q9ark8 paeonia ano
188	6	1.8	44	2	Q9ZFC8	Q9zfc8 lactococcus
189	6	1.8	44	10	Q9AQX1	Q9aqx1 paeonia obo
190	6	1.8	44	10	Q9AQX0	Q9aqx0 paeonia jap
191	6	1.8	44	10	Q9AQW9	Q9aqw9 paeonia mai
192	6	1.8	44	10	Q9AQW8	Q9aqw8 paeonia lut
193	6	1.8	44	10	Q9AQW7	Q9aqw7 paeonia del
194	6	1.8	44	10	Q9AQW6	Q9aqw6 paeonia roc
195	6	1.8	44	10	Q9AQW5	Q9aqw5 paeonia cal
196	6	1.8	44	10	Q9ARK7	Q9ark7 paeonia ano
197	6	1.8	44	10	Q9ARK5	Q9ark5 paeonia ten
198	6	1.8	44	10	Q9ARJ9	Q9arj9 paeonia lut
199	6	1.8	44	10	Q9ARJ8	Q9arj8 paeonia lut
200	6	1.8	44	10	Q9ARJ6	Q9arj6 paeonia del
201	6	1.8	44	10	Q9ARJ4	Q9arj4 paeonia suf
202	6	1.8	44	10	Q9ARJ3	Q9arj3 paeonia sze
203	6	1.8	44	10	Q9ARJ2	Q9arj2 paeonia sze
204	6	1.8	50	11	Q9QZJ9	Q9qzj9 cavia porce
205	6	1.8	52	10	Q9S8R6	Q9s8r6 helianthus
206	6	1.8	53	12	Q9JE44	Q9je44 human calic
207	6	1.8	53	12	Q9JA01	Q9ja01 human calic
208	6	1.8	53	16	Q9PAM9	Q9pam9 xylella fas
209	6	1.8	54	4	Q16487	Q16487 homo sapien
210	6	1.8	54	5	Q9TWZ0	Q9twz0 paramecium
211	6	1.8	56	11	Q9QZK0	Q9qzk0 cavia porce
212	6	1.8	57	5	Q9VQU6	Q9vqu6 drosophila
213	6	1.8	57	16	Q9PEL1	Q9pel1 xylella fas
214	6	1.8	61	2	Q9S316	Q9s316 rhodopseudo
215	6	1.8	63	5	Q9GPH6	Q9gph6 callosobruc
216	6	1.8	70	16	Q9K9J0	Q9k9j0 bacillus ha
217	6	1.8	71	2	P77799	P77799 rhodocyclus
218	6	1.8	71	2	Q9F5M3	Q9f5m3 rhodocyclus
219	6	1.8	73	16	Q97RA1	Q97ra1 streptococc
220	6	1.8	74	11	Q9QZK1	Q9qzk1 cavia porce
221	6	1.8	74	16	Q9CJV7	Q9cjv7 pasteurella
222	6	1.8	74	17	Q97BS5	Q97bs5 thermoplasm
223	6	1.8	75	4	Q9UDV4	Q9udv4 homo sapien
224	6	1.8	75	10	Q941N5	Q941n5 phytophthor
225	6	1.8	75	16	Q928Y4	Q928y4 listeria in
226	6	1.8	77	6	P79199	P79199 ovis aries
227	6	1.8	79	2	Q9AEV9	Q9aev9 lactococcus
228	6	1.8	79	5	Q9NE77	Q9ne77 leishmania
229	6	1.8	80	16	Q9A1Z4	Q9a1z4 streptococc
230	6	1.8	82	6	O46622	O46622 ceratotheri
231	6	1.8	87	12	Q9Q2T9	Q9q2t9 norwalk-lik
232	6	1.8	88	2	Q93H60	Q93h60 streptomyce
233	6	1.8	88	10	Q93YL8	Q93yl8 brassica ju
234	6	1.8	88	12	Q911T6	Q911t6 rabies viru
235	6	1.8	88	15	Q76015	Q76015 human immun

236	6	1.8	88	15	Q76016	Q76016 human immun
237	6	1.8	90	15	O41568	O41568 human immun
238	6	1.8	90	16	Q9RWZ8	Q9rwz8 deinococcus
239	6	1.8	91	6	Q9GM24	Q9gm24 macaca fasc
240	6	1.8	91	12	Q98516	Q98516 paramecium
241	6	1.8	92	2	Q51557	Q51557 pseudomonas
242	6	1.8	92	16	Q9X216	Q9x216 thermotoga
243	6	1.8	92	17	Q9YAL1	Q9yal1 aeropyrum p
244	6	1.8	94	16	Q9PH45	Q9ph45 xylella fas
245	6	1.8	96	2	Q51612	Q51612 unidentifie
246	6	1.8	96	15	O40298	O40298 human immun
247	6	1.8	97	16	O53672	O53672 mycobacteri
248	6	1.8	97	16	Q98M37	Q98m37 rhizobium l
249	6	1.8	98	16	O69509	O69509 mycobacteri
250	6	1.8	100	2	Q9X8E4	Q9x8e4 streptomyce
251	6	1.8	100	16	Q9PLT4	Q9plt4 chlamydia m
252	6	1.8	100	17	Q9YDH4	Q9ydh4 aeropyrum p
253	6	1.8	101	10	Q9ARA4	Q9ara4 linum usita
254	6	1.8	102	2	Q9RQY9	Q9rqy9 mycobacteri
255	6	1.8	102	16	Q989J3	Q989j3 rhizobium l
256	6	1.8	103	16	Q9PDN9	Q9pdn9 xylella fas
257	6	1.8	104	2	Q9K5H9	Q9k5h9 bordetella
258	6	1.8	105	2	Q9K5H7	Q9k5h7 bordetella
259	6	1.8	105	2	Q9K5G5	Q9k5g5 bordetella
260	6	1.8	105	3	Q9Y7H2	Q9y7h2 piromyces s
261	6	1.8	105	8	Q9XQR1	Q9xqr1 oryza sativ
262	6	1.8	105	8	Q9TJS7	Q9tjs7 oryza sativ
263	6	1.8	105	8	Q9TJS6	Q9tjs6 oryza sativ
264	6	1.8	105	9	Q9B055	Q9b055 mycobacteri
265	6	1.8	107	2	Q9R3B4	Q9r3b4 pseudomonas
266	6	1.8	107	2	Q9K5H5	Q9k5h5 bordetella
267	6	1.8	107	2	Q9K5G4	Q9k5g4 bordetella
268	6	1.8	107	2	Q9K5G1	Q9k5g1 bordetella
269	6	1.8	108	10	O82328	O82328 arabidopsis
270	6	1.8	109	2	Q9AJH0	Q9ajh0 vibrio prot
271	6	1.8	109	2	Q9K5H1	Q9k5h1 bordetella
272	6	1.8	109	6	Q9BE33	Q9be33 macaca fasc
273	6	1.8	110	6	Q9TUL1	Q9tul1 macaca mula
274	6	1.8	110	12	Q9IR98	Q9ir98 japanese ir
275	6	1.8	110	17	Q9YCL0	Q9ycl0 aeropyrum p
276	6	1.8	111	2	Q9K5G9	Q9k5g9 bordetella
277	6	1.8	111	2	Q9K5G7	Q9k5g7 bordetella
278	6	1.8	112	16	Q97PD1	Q97pd1 streptococc
279	6	1.8	112	17	Q9YEH9	Q9yeh9 aeropyrum p
280	6	1.8	115	2	Q9KJY1	Q9kjy1 bordetella
281	6	1.8	115	2	Q9KJY0	Q9kjy0 bordetella
282	6	1.8	115	2	Q9K5H3	Q9k5h3 bordetella
283	6	1.8	116	5	Q9GR25	Q9gr25 nematostell
284	6	1.8	116	5	Q9BN62	Q9bn62 proscotolem
285	6	1.8	116	12	Q914J8	Q914j8 sulfolobus
286	6	1.8	117	5	Q9W398	Q9w398 drosophila
287	6	1.8	117	16	O32022	O32022 bacillus su
288	6	1.8	118	9	Q9ZX36	Q9zx36 mycobacteri
289	6	1.8	118	15	Q76140	Q76140 human immun
290	6	1.8	118	16	Q9RVI4	Q9rvi4 deinococcus
291	6	1.8	122	2	Q9KJX9	Q9kjx9 bordetella
292	6	1.8	122	16	O06749	O06749 bacillus su
293	6	1.8	124	2	Q9R7L2	Q9r7l2 unidentifie
294	6	1.8	124	2	Q9R7L1	Q9r7l1 unidentifie
295	6	1.8	124	4	Q96SC7	Q96sc7 homo sapien
296	6	1.8	127	10	Q9ZSV5	Q9zsv5 acetabulari
297	6	1.8	127	15	Q9QMA8	Q9qma8 human immun
298	6	1.8	127	16	Q9JXR0	Q9jxr0 neisseria m
299	6	1.8	127	16	Q92US6	Q92us6 rhizobium m
300	6	1.8	128	5	O61215	O61215 caenorhabdi
301	6	1.8	128	15	P89632	P89632 human immun
302	6	1.8	129	4	Q9NVV2	Q9nvv2 homo sapien
303	6	1.8	129	15	Q66004	Q66004 caprine art
304	6	1.8	129	16	Q92F99	Q92f99 listeria in
305	6	1.8	131	2	P72545	P72545 synechococc
306	6	1.8	132	12	O41075	O41075 paramecium
307	6	1.8	134	2	Q9F5F1	Q9f5f1 agrobacteri
308	6	1.8	134	11	Q9CRZ2	Q9crz2 mus musculu
309	6	1.8	134	16	Q9JZM1	Q9jzm1 neisseria m
310	6	1.8	135	5	Q9NCN9	Q9ncn9 giardia lam
311	6	1.8	135	16	O05840	O05840 mycobacteri
312	6	1.8	136	10	Q9LNZ7	Q9lnz7 arabidopsis
313	6	1.8	136	16	Q9I0G4	Q9i0g4 pseudomonas
314	6	1.8	137	2	Q9FBW4	Q9fbw4 streptomyce
315	6	1.8	138	5	Q9NCK9	Q9nck9 drosophila
316	6	1.8	138	5	Q9NCK8	Q9nck8 drosophila
317	6	1.8	138	5	Q9NCK7	Q9nck7 drosophila
318	6	1.8	138	10	Q94DU2	Q94du2 oryza sativ
319	6	1.8	138	16	Q92VU3	Q92vu3 rhizobium m
320	6	1.8	138	17	Q975T1	Q975t1 sulfolobus
321	6	1.8	139	4	Q9BST1	Q9bst1 homo sapien
322	6	1.8	139	4	Q9NWK0	Q9nwk0 homo sapien
323	6	1.8	139	16	Q9JUQ5	Q9juq5 neisseria m
324	6	1.8	139	16	Q9JS11	Q9js11 neisseria m
325	6	1.8	141	4	Q9NXX4	Q9nxx4 homo sapien
326	6	1.8	141	17	Q975J0	Q975j0 sulfolobus
327	6	1.8	143	16	Q9ZCF0	Q9zcf0 rickettsia
328	6	1.8	143	16	Q9KBG7	Q9kbg7 bacillus ha
329	6	1.8	144	2	Q9RHG3	Q9rhg3 mycobacteri
330	6	1.8	144	2	O52206	O52206 morganella
331	6	1.8	144	2	O52210	O52210 serratia ma
332	6	1.8	144	10	Q9LJ53	Q9lj53 arabidopsis
333	6	1.8	145	17	Q9HN94	Q9hn94 halobacteri
334	6	1.8	146	11	Q60482	Q60482 cavia porce
335	6	1.8	147	1	Q9C4V2	Q9c4v2 sulfolobus
336	6	1.8	147	2	Q9ACX7	Q9acx7 streptomyce
337	6	1.8	147	11	Q9CY54	Q9cy54 mus musculu
338	6	1.8	147	11	Q9CY12	Q9cy12 mus musculu
339	6	1.8	147	11	Q9CXH5	Q9cxh5 mus musculu
340	6	1.8	147	11	Q91V86	Q91v86 m 11 days e
341	6	1.8	147	17	Q9YF58	Q9yf58 aeropyrum p
342	6	1.8	148	1	O93698	O93698 sulfolobus
343	6	1.8	148	2	O66226	O66226 synechococc
344	6	1.8	148	4	O75575	O75575 homo sapien
345	6	1.8	148	10	O24162	O24162 nicotiana t
346	6	1.8	148	17	Q9UZI0	Q9uzi0 pyrococcus
347	6	1.8	150	5	Q9W026	Q9w026 drosophila
348	6	1.8	151	16	Q9KLP9	Q9klp9 vibrio chol
349	6	1.8	154	2	Q52578	Q52578 pseudomonas
350	6	1.8	154	2	Q52592	Q52592 agrobacteri
351	6	1.8	155	2	Q9EVQ3	Q9evq3 escherichia
352	6	1.8	155	2	Q9JPF3	Q9jpf3 neisseria m
353	6	1.8	155	4	Q9P0R6	Q9p0r6 homo sapien
354	6	1.8	155	11	P70440	P70440 mus musculu
355	6	1.8	155	12	Q86797	Q86797 turkey herp
356	6	1.8	155	12	Q69310	Q69310 gallid herp
357	6	1.8	156	3	Q9P7J9	Q9p7j9 schizosacch
358	6	1.8	156	5	Q18878	Q18878 caenorhabdi
359	6	1.8	156	8	Q9TLV7	Q9tlv7 cyanidium c
360	6	1.8	157	2	Q47443	Q47443 escherichia
361	6	1.8	158	10	Q940Z3	Q940z3 arabidopsis
362	6	1.8	159	5	Q9VIL5	Q9vil5 drosophila
363	6	1.8	159	10	Q9LF40	Q9lf40 arabidopsis
364	6	1.8	160	5	Q94443	Q94443 chironomus
365	6	1.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
366	6	1.8	160	16	Q92WL4	Q92wl4 rhizobium m
367	6	1.8	160	17	Q980M4	Q980m4 sulfolobus
368	6	1.8	161	2	O30617	O30617 myxococcus
369	6	1.8	161	5	Q94445	Q94445 chironomus
370	6	1.8	161	5	O02368	O02368 chironomus
371	6	1.8	161	16	Q9FBC1	Q9fbc1 streptococc
372	6	1.8	161	16	Q929W5	Q929w5 listeria in
373	6	1.8	162	5	Q25217	Q25217 kiefferulus
374	6	1.8	162	5	Q25218	Q25218 kiefferulus
375	6	1.8	162	5	Q25219	Q25219 kiefferulus
376	6	1.8	163	2	Q9L559	Q9l559 pseudomonas
377	6	1.8	163	5	O45848	O45848 caenorhabdi
378	6	1.8	163	11	Q9CXZ2	Q9cxz2 mus musculu
379	6	1.8	164	2	O30747	O30747 rhodobacter
380	6	1.8	164	4	Q9NV35	Q9nv35 homo sapien
381	6	1.8	164	9	Q9MCD9	Q9mcd9 bacteriopha

382	6	1.8	165	8	Q950T3	Q950t3 hyaloraphid
383	6	1.8	165	16	Q98IV8	Q98iv8 rhizobium l
384	6	1.8	165	17	Q96YF0	Q96yf0 sulfolobus
385	6	1.8	166	2	Q9ZIM5	Q9zim5 listeria mo
386	6	1.8	166	4	Q9H8L8	Q9h8l8 homo sapien
387	6	1.8	166	10	Q9FGA5	Q9fga5 arabidopsis
388	6	1.8	166	16	Q928N5	Q928n5 listeria in
389	6	1.8	167	16	Q9PAS8	Q9pas8 xylella fas
390	6	1.8	168	2	Q9S6K2	Q9s6k2 campylobact
391	6	1.8	168	10	Q9XF96	Q9xf96 prunus arme
392	6	1.8	168	10	Q9SM77	Q9sm77 oryza sativ
393	6	1.8	168	16	Q92SI5	Q92si5 rhizobium m
394	6	1.8	169	11	Q64614	Q64614 rattus norv
395	6	1.8	169	16	Q9K7E0	Q9k7e0 bacillus ha
396	6	1.8	170	4	Q9BWS8	Q9bws8 homo sapien
397	6	1.8	170	4	Q9P0W6	Q9p0w6 homo sapien
398	6	1.8	170	10	Q9SYP8	Q9syp8 arabidopsis
399	6	1.8	172	10	O80393	O80393 mesembryant
400	6	1.8	172	13	Q9I9J6	Q9i9j6 gallus gall
401	6	1.8	172	13	Q90368	Q90368 coturnix co
402	6	1.8	173	10	Q9M4H7	Q9m4h7 vitis vinif
403	6	1.8	174	5	Q20138	Q20138 caenorhabdi
404	6	1.8	175	4	O95994	O95994 homo sapien
405	6	1.8	175	10	O23011	O23011 arabidopsis
406	6	1.8	175	11	O88312	O88312 mus musculu
407	6	1.8	176	11	Q9JJU3	Q9jju3 mus musculu
408	6	1.8	176	16	Q98DU4	Q98du4 rhizobium l
409	6	1.8	177	10	Q9AS02	Q9as02 oryza sativ
410	6	1.8	178	5	Q9BH30	Q9bh30 bombyx mori
411	6	1.8	178	11	Q9QZR7	Q9qzr7 mus musculu
412	6	1.8	180	17	Q9YDT6	Q9ydt6 aeropyrum p
413	6	1.8	180	17	Q979H7	Q979h7 thermoplasm
414	6	1.8	181	5	O44095	O44095 drosophila
415	6	1.8	181	16	Q9I341	Q9i341 pseudomonas
416	6	1.8	182	5	Q95RZ9	Q95rz9 drosophila
417	6	1.8	183	11	Q9CWA7	Q9cwa7 mus musculu
418	6	1.8	183	15	Q90CQ4	Q90cq4 human immun
419	6	1.8	184	8	Q9MGB6	Q9mgb6 chrysodidym
420	6	1.8	185	4	Q9HBP9	Q9hbp9 homo sapien
421	6	1.8	185	5	P91455	P91455 caenorhabdi
422	6	1.8	186	2	Q9Z667	Q9z667 zymomonas m
423	6	1.8	186	10	Q9LID5	Q9lid5 arabidopsis
424	6	1.8	187	2	Q9JRM0	Q9jrm0 xanthomonas
425	6	1.8	187	2	Q9JRL9	Q9jrl9 xanthomonas
426	6	1.8	187	2	Q9JRL8	Q9jrl8 xanthomonas
427	6	1.8	187	2	Q9JRL7	Q9jrl7 xanthomonas
428	6	1.8	187	10	Q9M692	Q9m692 gossypioide
429	6	1.8	188	2	Q9S691	Q9s691 haemophilus
430	6	1.8	188	2	Q9S6A5	Q9s6a5 haemophilus
431	6	1.8	188	2	Q9S6A6	Q9s6a6 haemophilus
432	6	1.8	188	2	Q9S6A9	Q9s6a9 haemophilus
433	6	1.8	188	3	Q9USC5	Q9usc5 schizosacch
434	6	1.8	189	2	Q9S6A4	Q9s6a4 haemophilus
435	6	1.8	189	16	Q9HZT7	Q9hzt7 pseudomonas
436	6	1.8	190	4	Q96IU0	Q96iu0 homo sapien
437	6	1.8	190	9	Q9ZXB6	Q9zxb6 bacteriopha
438	6	1.8	190	17	Q97Z57	Q97z57 sulfolobus
439	6	1.8	191	4	Q9H2R0	Q9h2r0 homo sapien
440	6	1.8	191	16	Q9KSL0	Q9ksl0 vibrio chol
441	6	1.8	191	17	Q9YBM4	Q9ybm4 aeropyrum p
442	6	1.8	192	5	Q9XYY6	Q9xyy6 leishmania
443	6	1.8	193	8	Q955G8	Q955g8 philautus c
444	6	1.8	194	10	Q943S3	Q943s3 oryza sativ
445	6	1.8	194	12	Q04393	Q04393 acholeplasm
446	6	1.8	194	16	Q9A1Q5	Q9a1q5 streptococc
447	6	1.8	195	4	O60532	O60532 homo sapien
448	6	1.8	196	12	Q918B7	Q918b7 norwalk-lik
449	6	1.8	196	12	Q918B1	Q918b1 norwalk-lik
450	6	1.8	196	12	Q918A8	Q918a8 norwalk-lik
451	6	1.8	197	2	Q9S2I2	Q9s2i2 streptomyce
452	6	1.8	197	8	Q9TBW2	Q9tbw2 acropora te
453	6	1.8	197	16	O53706	O53706 mycobacteri
454	6	1.8	197	16	Q9KCJ7	Q9kcj7 bacillus ha
455	6	1.8	198	2	Q9AHP0	Q9ahp0 bordetella
456	6	1.8	198	10	Q9C7Y9	Q9c7y9 arabidopsis
457	6	1.8	199	10	Q9SFU5	Q9sfu5 arabidopsis
458	6	1.8	200	2	Q9RK54	Q9rk54 streptomyce
459	6	1.8	200	2	Q9ALP9	Q9alp9 bordetella
460	6	1.8	200	12	Q9DJ41	Q9dj41 spodoptera
461	6	1.8	200	16	Q9A6T1	Q9a6t1 caulobacter
462	6	1.8	202	17	Q973S3	Q973s3 sulfolobus
463	6	1.8	203	4	Q96GR5	Q96gr5 homo sapien
464	6	1.8	203	5	O18036	O18036 caenorhabdi
465	6	1.8	203	10	Q9SFU7	Q9sfu7 arabidopsis
466	6	1.8	203	16	Q9PIJ4	Q9pij4 campylobact
467	6	1.8	204	8	Q37397	Q37397 allomyces m
468	6	1.8	204	12	Q9ICG6	Q9icg6 white spot
469	6	1.8	204	13	O13225	O13225 poeciliopsi
470	6	1.8	205	17	Q9V1M7	Q9v1m7 pyrococcus
471	6	1.8	206	4	Q96JY2	Q96jy2 homo sapien
472	6	1.8	208	10	Q9LYM3	Q9lym3 arabidopsis
473	6	1.8	208	16	Q9PER6	Q9per6 xylella fas
474	6	1.8	209	2	Q9L593	Q9l593 streptococc
475	6	1.8	212	11	Q9CRJ0	Q9crj0 mus musculu
476	6	1.8	213	2	Q9X6F5	Q9x6f5 campylobact
477	6	1.8	213	2	Q9X6F6	Q9x6f6 campylobact
478	6	1.8	213	2	Q9X6F7	Q9x6f7 campylobact
479	6	1.8	213	5	Q9GTY8	Q9gty8 plasmodium
480	6	1.8	213	10	Q9C782	Q9c782 arabidopsis
481	6	1.8	213	11	Q9D3J8	Q9d3j8 mus musculu
482	6	1.8	213	16	Q9I234	Q9i234 pseudomonas
483	6	1.8	214	11	Q9R0Q8	Q9r0q8 mus musculu
484	6	1.8	214	12	Q91PQ3	Q91pq3 tt virus. o
485	6	1.8	215	2	Q9ALQ4	Q9alq4 bordetella
486	6	1.8	215	16	Q9RT89	Q9rt89 deinococcus
487	6	1.8	215	17	Q9HMZ7	Q9hmz7 halobacteri
488	6	1.8	216	6	Q9BDH3	Q9bdh3 sus scrofa
489	6	1.8	216	11	Q9D440	Q9d440 mus musculu
490	6	1.8	216	12	Q9QC02	Q9qc02 simian cyto
491	6	1.8	216	16	Q97M23	Q97m23 clostridium
492	6	1.8	217	16	Q9CEW9	Q9cew9 lactococcus
493	6	1.8	217	16	Q99ZG6	Q99zg6 streptococc
494	6	1.8	217	16	Q97Q36	Q97q36 streptococc
495	6	1.8	218	17	Q975M7	Q975m7 sulfolobus
496	6	1.8	219	5	Q962U1	Q962u1 spodoptera
497	6	1.8	219	10	Q9ZTW3	Q9ztw3 arabidopsis
498	6	1.8	219	14	Q91US0	Q91us0 plasmid psb
499	6	1.8	219	16	Q9A2Y3	Q9a2y3 caulobacter
500	6	1.8	219	17	Q9V1Z4	Q9v1z4 pyrococcus
501	6	1.8	221	5	Q9NEU2	Q9neu2 caenorhabdi
502	6	1.8	222	2	Q9LBQ2	Q9lbq2 mycobacteri
503	6	1.8	222	2	Q9L584	Q9l584 streptococc
504	6	1.8	222	2	Q9L577	Q9l577 streptococc
505	6	1.8	222	5	O01786	O01786 caenorhabdi
506	6	1.8	223	16	Q9A740	Q9a740 caulobacter
507	6	1.8	223	17	Q96XA5	Q96xa5 sulfolobus
508	6	1.8	224	2	Q9KKH2	Q9kkh2 yersinia en
509	6	1.8	224	2	Q9S1Q0	Q9s1q0 streptomyce
510	6	1.8	224	2	Q93NK7	Q93nk7 yersinia en
511	6	1.8	224	4	O00309	O00309 homo sapien
512	6	1.8	224	10	Q40760	Q40760 picea abies
513	6	1.8	225	2	Q9L591	Q9l591 streptococc
514	6	1.8	225	16	Q98PT4	Q98pt4 mycoplasma
515	6	1.8	226	12	Q98260	Q98260 molluscum c
516	6	1.8	227	2	Q9KGS0	Q9kgs0 streptococc
517	6	1.8	227	5	O00924	O00924 plasmodium
518	6	1.8	227	5	Q9GTY7	Q9gty7 plasmodium
519	6	1.8	227	8	Q9B6X7	Q9b6x7 crypturellu
520	6	1.8	227	10	Q94AY4	Q94ay4 arabidopsis
521	6	1.8	227	16	O06556	O06556 mycobacteri
522	6	1.8	228	2	Q9L5B8	Q9l5b8 streptococc
523	6	1.8	228	8	Q9MLZ5	Q9mlz5 sceloporus
524	6	1.8	228	11	Q923S7	Q923s7 rattus norv
525	6	1.8	228	16	Q9A306	Q9a306 caulobacter
526	6	1.8	228	16	Q97MP4	Q97mp4 clostridium
527	6	1.8	228	17	O27259	O27259 methanother

528	6	1.8	228	17	Q9HSL4	Q9hsl4 halobacteri
529	6	1.8	229	8	Q9MLZ4	Q9mlz4 sceloporus
530	6	1.8	229	16	Q98KC5	Q98kc5 rhizobium l
531	6	1.8	230	16	Q9PB87	Q9pb87 xylella fas
532	6	1.8	231	2	O06030	O06030 lactococcus
533	6	1.8	231	2	Q9L579	Q91579 streptococc
534	6	1.8	231	2	Q9ALP3	Q9alp3 bordetella
535	6	1.8	231	8	Q9G5K2	Q9g5k2 anolis marm
536	6	1.8	231	8	Q9G5J4	Q9g5j4 anolis marm
537	6	1.8	231	8	Q9G5J3	Q9g5j3 anolis ocul
538	6	1.8	231	8	Q9G5J2	Q9g5j2 anolis livi
539	6	1.8	231	10	Q9SNT9	Q9snt9 oryza sativ
540	6	1.8	231	16	Q9I079	Q9i079 pseudomonas
541	6	1.8	232	5	O16890	O16890 caenorhabdi
542	6	1.8	232	12	Q89398	Q89398 paramecium
543	6	1.8	232	16	Q92MU1	Q92mu1 rhizobium m
544	6	1.8	232	17	O57773	O57773 pyrococcus
545	6	1.8	234	10	O48529	O48529 arabidopsis
546	6	1.8	234	16	Q99YB2	Q99yb2 streptococc
547	6	1.8	235	2	Q9L582	Q91582 streptococc
548	6	1.8	236	2	Q9ZAM2	Q9zam2 sphingomona
549	6	1.8	237	2	Q9L592	Q91592 streptococc
550	6	1.8	237	5	Q19860	Q19860 caenorhabdi
551	6	1.8	237	16	Q97R52	Q97r52 streptococc
552	6	1.8	238	16	O66599	O66599 aquifex aeo
553	6	1.8	238	16	Q9K7T6	Q9k7t6 bacillus ha
554	6	1.8	239	2	Q49014	Q49014 mycoplasma
555	6	1.8	239	16	Q97MW9	Q97mw9 clostridium
556	6	1.8	239	17	Q9YAS7	Q9yas7 aeropyrum p
557	6	1.8	241	2	Q9L580	Q91580 streptococc
558	6	1.8	241	5	Q9VA32	Q9va32 drosophila
559	6	1.8	241	16	P73234	P73234 synechocyst
560	6	1.8	242	2	Q9L562	Q91562 streptococc
561	6	1.8	242	2	Q44929	Q44929 bacillus br
562	6	1.8	242	4	Q96N48	Q96n48 homo sapien
563	6	1.8	242	16	Q98F24	Q98f24 rhizobium l
564	6	1.8	243	10	Q9SDB8	Q9sdb8 oryza sativ
565	6	1.8	243	11	Q61303	Q61303 mus musculu
566	6	1.8	245	4	Q9UQK7	Q9uqk7 homo sapien
567	6	1.8	245	12	Q69127	Q69127 human herpe
568	6	1.8	245	16	Q9X101	Q9x101 thermotoga
569	6	1.8	245	16	Q9CB46	Q9cb46 mycobacteri
570	6	1.8	246	2	Q9L5B4	Q915b4 streptococc
571	6	1.8	246	2	Q9L578	Q91578 streptococc
572	6	1.8	246	6	Q95LW4	Q95lw4 macaca fasc
573	6	1.8	247	6	Q9BDH4	Q9bdh4 sus scrofa
574	6	1.8	247	16	Q9I040	Q9i040 pseudomonas
575	6	1.8	249	2	Q9L5D4	Q915d4 streptococc
576	6	1.8	249	2	Q9L5B7	Q915b7 streptococc
577	6	1.8	249	2	Q9L585	Q91585 streptococc
578	6	1.8	249	3	Q06672	Q06672 saccharomyc
579	6	1.8	249	16	Q98M22	Q98m22 rhizobium l
580	6	1.8	250	4	Q9BQ58	Q9bq58 homo sapien
581	6	1.8	250	5	Q9VKG7	Q9vkg7 drosophila
582	6	1.8	251	4	Q9NXA0	Q9nxa0 homo sapien
583	6	1.8	251	10	O49473	O49473 arabidopsis
584	6	1.8	252	2	Q9L583	Q91583 streptococc
585	6	1.8	252	2	Q9ALQ2	Q9alq2 bordetella
586	6	1.8	253	2	P94626	P94626 clostridium
587	6	1.8	253	10	O22082	O22082 petunia hyb
588	6	1.8	253	11	Q9DBJ0	Q9dbj0 mus musculu
589	6	1.8	253	16	P94382	P94382 bacillus su
590	6	1.8	253	17	O27406	O27406 methanother
591	6	1.8	254	2	Q9K3Y6	Q9k3y6 streptomyce
592	6	1.8	254	4	O60768	O60768 homo sapien
593	6	1.8	255	2	Q9L5B6	Q915b6 streptococc
594	6	1.8	255	2	Q9L581	Q91581 streptococc
595	6	1.8	256	2	Q9L595	Q91595 streptococc
596	6	1.8	256	2	Q9L590	Q91590 streptococc
597	6	1.8	256	2	Q9ALQ0	Q9alq0 bordetella
598	6	1.8	256	16	Q98K73	Q98k73 rhizobium l
599	6	1.8	257	2	Q9L594	Q91594 streptococc
600	6	1.8	257	16	Q99Y11	Q99y11 streptococc
601	6	1.8	258	12	Q98444	Q98444 paramecium
602	6	1.8	258	17	O29264	O29264 archaeoglob
603	6	1.8	259	4	Q96EE0	Q96ee0 homo sapien
604	6	1.8	260	2	P71102	P71102 curtobacter
605	6	1.8	260	2	Q52548	Q52548 pseudomonas
606	6	1.8	260	5	Q9VRD1	Q9vrd1 drosophila
607	6	1.8	260	7	Q06744	Q06744 xenopus lae
608	6	1.8	260	7	Q06746	Q06746 xenopus lae
609	6	1.8	261	5	Q25240	Q25240 leishmania
610	6	1.8	261	5	P91279	P91279 caenorhabdi
611	6	1.8	261	11	Q9QUP7	Q9qup7 mus musculu
612	6	1.8	261	16	Q92AE6	Q92ae6 listeria in
613	6	1.8	262	2	Q9L576	Q91576 streptococc
614	6	1.8	262	10	Q9SWC5	Q9swc5 betula verr
615	6	1.8	262	11	O88346	O88346 mus musculu
616	6	1.8	262	12	Q918P3	Q918p3 bovine herp
617	6	1.8	263	3	O74316	O74316 schizosacch
618	6	1.8	263	5	Q9VMK3	Q9vmk3 drosophila
619	6	1.8	263	10	Q9LVL9	Q91vl9 arabidopsis
620	6	1.8	264	12	Q9YMT0	Q9ymt0 lymantria d
621	6	1.8	264	16	Q98K02	Q98k02 rhizobium l
622	6	1.8	264	16	P71701	P71701 mycobacteri
623	6	1.8	265	10	Q9LTP9	Q91tp9 arabidopsis
624	6	1.8	266	6	Q95KD6	Q95kd6 macaca fasc
625	6	1.8	266	10	Q9FF65	Q9ff65 arabidopsis
626	6	1.8	266	10	Q93VE7	Q93ve7 arabidopsis
627	6	1.8	266	16	Q9PP58	Q9pp58 campylobact
628	6	1.8	267	2	Q9RNL1	Q9rnl1 zymomonas m
629	6	1.8	267	2	O05150	O05150 rhodococcus
630	6	1.8	267	8	Q94W05	Q94w05 plecotus au
631	6	1.8	267	12	O56823	O56823 human cytom
632	6	1.8	267	12	O56824	O56824 human cytom
633	6	1.8	267	12	O56825	O56825 human cytom
634	6	1.8	267	12	O56829	O56829 human cytom
635	6	1.8	267	13	O73909	O73909 gallus gall
636	6	1.8	268	5	Q26561	Q26561 schistosoma
637	6	1.8	268	12	O56826	O56826 human cytom
638	6	1.8	268	16	Q9I4N2	Q9i4n2 pseudomonas
639	6	1.8	269	2	Q9KZC3	Q9kzc3 streptomyce
640	6	1.8	269	2	Q46097	Q46097 campylobact
641	6	1.8	269	7	Q06742	Q06742 xenopus lae
642	6	1.8	269	7	Q06743	Q06743 xenopus lae
643	6	1.8	269	8	Q950L8	Q95018 rhizophydiu
644	6	1.8	269	17	Q9YBA6	Q9yba6 aeropyrum p
645	6	1.8	270	2	Q9R6V2	Q9r6v2 synechococc
646	6	1.8	270	2	O34158	O34158 salmonella
647	6	1.8	270	3	Q12253	Q12253 saccharomyc
648	6	1.8	270	7	Q06745	Q06745 xenopus lae
649	6	1.8	270	11	Q9D8G2	Q9d8g2 mus musculu
650	6	1.8	270	16	Q92UX0	Q92ux0 rhizobium m
651	6	1.8	271	5	Q9U1D5	Q9uld5 leishmania
652	6	1.8	271	16	Q9I6U7	Q9i6u7 pseudomonas
653	6	1.8	271	16	Q98JG9	Q98jg9 rhizobium l
654	6	1.8	272	4	Q9BWR0	Q9bwr0 homo sapien
655	6	1.8	272	5	Q9BJW6	Q9bjw6 sarsia sp.
656	6	1.8	272	12	O56827	O56827 human cytom
657	6	1.8	273	5	Q95Y76	Q95y76 caenorhabdi
658	6	1.8	273	16	Q9K0I1	Q9k0i1 neisseria m
659	6	1.8	273	16	Q9JVI4	Q9jvi4 neisseria m
660	6	1.8	273	17	O58086	O58086 pyrococcus
661	6	1.8	273	17	Q9HP49	Q9hp49 halobacteri
662	6	1.8	274	16	Q9HYG4	Q9hyg4 pseudomonas
663	6	1.8	274	17	Q96YU1	Q96yu1 sulfolobus
664	6	1.8	275	3	P78840	P78840 schizosacch
665	6	1.8	275	5	Q9U9C3	Q9u9c3 caenorhabdi
666	6	1.8	275	5	Q9XW88	Q9xw88 caenorhabdi
667	6	1.8	275	11	Q9JLE2	Q9jle2 mus musculu
668	6	1.8	275	12	O36368	O36368 alcelaphine
669	6	1.8	276	5	Q9VHW6	Q9vhw6 drosophila
670	6	1.8	276	16	Q92V63	Q92v63 rhizobium m
671	6	1.8	277	5	Q9NEI3	Q9nei3 caenorhabdi
672	6	1.8	277	5	Q27045	Q27045 theileria p
673	6	1.8	278	16	Q9HTB1	Q9htb1 pseudomonas

674	6	1.8	280	10	Q94LQ8	Q94lq8 oryza sativ
675	6	1.8	281	4	Q96P12	Q96p12 homo sapien
676	6	1.8	281	16	O84203	O84203 chlamydia t
677	6	1.8	284	11	Q9CZL3	Q9czl3 mus musculu
678	6	1.8	284	16	Q9K6I3	Q9k6i3 bacillus ha
679	6	1.8	285	5	Q17453	Q17453 caenorhabdi
680	6	1.8	285	11	Q9CY28	Q9cy28 mus musculu
681	6	1.8	286	5	Q9GU36	Q9gu36 trypanosoma
682	6	1.8	286	16	Q9CKX6	Q9ckx6 pasteurella
683	6	1.8	286	16	Q9CCW1	Q9ccw1 mycobacteri
684	6	1.8	287	2	Q9RLJ6	Q9rlj6 oenococcus
685	6	1.8	287	2	Q9RLJ5	Q9rlj5 oenococcus
686	6	1.8	287	2	Q93QX1	Q93qx1 corynebacte
687	6	1.8	287	13	Q91002	Q91002 gallus gall
688	6	1.8	287	16	Q9PKJ2	Q9pkj2 chlamydia m
689	6	1.8	288	3	Q03430	Q03430 saccharomyc
690	6	1.8	288	5	Q9W104	Q9w104 drosophila
691	6	1.8	288	12	Q9IGT9	Q9igt9 porcine ade
692	6	1.8	288	17	Q58591	Q58591 methanococc
693	6	1.8	289	2	Q9KZ73	Q9kz73 streptomyce
694	6	1.8	289	12	Q91H10	Q91h10 human calic
695	6	1.8	290	12	Q89483	Q89483 gallid herp
696	6	1.8	290	12	Q86876	Q86876 gallid herp
697	6	1.8	290	12	Q69304	Q69304 marek's dis
698	6	1.8	291	2	Q9K4G6	Q9k4g6 streptomyce
699	6	1.8	291	2	Q93TU0	Q93tu0 acidithioba
700	6	1.8	291	11	Q91XF6	Q91xf6 mus musculu
701	6	1.8	291	16	Q9CL10	Q9cl10 pasteurella
702	6	1.8	291	16	Q929F4	Q929f4 listeria in
703	6	1.8	291	17	Q96X95	Q96x95 sulfolobus
704	6	1.8	292	3	Q96WP1	Q96wp1 agaricus bi
705	6	1.8	292	13	Q9YGW4	Q9ygw4 gallus gall
706	6	1.8	293	3	O94627	O94627 schizosacch
707	6	1.8	293	10	Q9AWY2	Q9awy2 oryza sativ
708	6	1.8	293	16	P73482	P73482 synechocyst
709	6	1.8	293	16	Q98D27	Q98d27 rhizobium l
710	6	1.8	294	5	O43946	O43946 sarcocystis
711	6	1.8	294	12	Q69225	Q69225 mouse cytom
712	6	1.8	294	16	Q9CP11	Q9cp11 pasteurella
713	6	1.8	294	17	Q9HLU7	Q9hlu7 thermoplasm
714	6	1.8	296	12	Q9DWE0	Q9dwe0 rat cytomeg
715	6	1.8	296	16	Q98KY0	Q98ky0 rhizobium l
716	6	1.8	296	16	Q984Z4	Q984z4 rhizobium l
717	6	1.8	297	2	Q9F1U9	Q9f1u9 'flavobacte
718	6	1.8	297	11	Q9CYH3	Q9cyh3 mus musculu
719	6	1.8	298	16	Q98QQ2	Q98qq2 mycoplasma
720	6	1.8	299	4	Q13059	Q13059 homo sapien
721	6	1.8	299	10	Q9SQ56	Q9sq56 nicotiana t
722	6	1.8	299	10	Q9SVC1	Q9svc1 arabidopsis
723	6	1.8	299	16	Q9KCP0	Q9kcp0 bacillus ha
724	6	1.8	299	17	O27045	O27045 methanother
725	6	1.8	300	2	Q93F72	Q93f72 bacillus sp
726	6	1.8	300	2	Q93F70	Q93f70 bacillus sp
727	6	1.8	300	4	Q15868	Q15868 homo sapien
728	6	1.8	300	5	Q9V4Q2	Q9v4q2 drosophila
729	6	1.8	300	10	Q39979	Q39979 hyoscyamus
730	6	1.8	300	16	Q929B2	Q929b2 listeria in
731	6	1.8	301	16	Q9WZ55	Q9wz55 thermotoga
732	6	1.8	301	16	Q9RW36	Q9rw36 deinococcus
733	6	1.8	301	16	Q9K9T1	Q9k9t1 bacillus ha
734	6	1.8	302	5	Q9GRK1	Q9grk1 leishmania
735	6	1.8	302	10	Q40734	Q40734 oryza sativ
736	6	1.8	303	5	Q22981	Q22981 caenorhabdi
737	6	1.8	303	16	O53566	O53566 mycobacteri
738	6	1.8	303	16	Q9HWR1	Q9hwr1 pseudomonas
739	6	1.8	304	2	Q9ALP7	Q9alp7 bordetella
740	6	1.8	305	2	Q9L259	Q91259 streptomyce
741	6	1.8	305	3	O94417	O94417 schizosacch
742	6	1.8	305	4	Q9H9S0	Q9h9s0 homo sapien
743	6	1.8	305	10	Q9ZWG1	Q9zwg1 arabidopsis
744	6	1.8	306	5	Q95SR5	Q95sr5 drosophila
745	6	1.8	306	16	Q98GP2	Q98gp2 rhizobium l
746	6	1.8	306	16	Q98BM0	Q98bm0 rhizobium l
747	6	1.8	307	2	P95407	P95407 pseudomonas
748	6	1.8	307	2	Q59709	Q59709 pseudomonas
749	6	1.8	307	2	Q59708	Q59708 pseudomonas
750	6	1.8	307	10	Q9AY72	Q9ay72 oryza sativ
751	6	1.8	307	10	Q9M030	Q9m030 arabidopsis
752	6	1.8	307	16	Q9CEX6	Q9cex6 lactococcus
753	6	1.8	307	17	O28263	O28263 archaeoglob
754	6	1.8	308	2	Q53509	Q53509 alcaligenes
755	6	1.8	308	10	Q9MA06	Q9ma06 arabidopsis
756	6	1.8	309	2	O87625	O87625 pseudomonas
757	6	1.8	309	10	Q9SSR0	Q9ssr0 arabidopsis
758	6	1.8	310	4	Q96SG6	Q96sg6 homo sapien
759	6	1.8	310	13	Q98T56	Q98t56 tockus eryt
760	6	1.8	310	17	Q9UXJ4	Q9uxj4 sulfolobus
761	6	1.8	311	5	Q9NF49	Q9nf49 drosophila
762	6	1.8	311	10	Q9FTR1	Q9ftr1 oryza sativ
763	6	1.8	311	12	Q91GC4	Q91gc4 epiphyas po
764	6	1.8	311	16	Q92SW2	Q92sw2 rhizobium m
765	6	1.8	312	5	O76577	O76577 caenorhabdi
766	6	1.8	312	11	Q9CW94	Q9cw94 mus musculu
767	6	1.8	312	16	Q98CQ9	Q98cq9 rhizobium l
768	6	1.8	313	5	Q95SU6	Q95su6 drosophila
769	6	1.8	314	8	Q9MD53	Q9md53 phytomonas
770	6	1.8	314	11	Q9EPG2	Q9epg2 mus musculu
771	6	1.8	315	6	O97601	O97601 oryctolagus
772	6	1.8	316	2	Q9AE41	Q9ae41 rhizobium l
773	6	1.8	316	5	Q9VC37	Q9vc37 drosophila
774	6	1.8	316	5	Q95PB3	Q95pb3 ascaris suu
775	6	1.8	316	10	Q9LJJ2	Q9ljj2 arabidopsis
776	6	1.8	316	10	P93323	P93323 medicago sa
777	6	1.8	317	5	Q95PB5	Q95pb5 ascaris suu
778	6	1.8	318	5	Q17090	Q17090 ascaris suu
779	6	1.8	318	5	Q95PB6	Q95pb6 ascaris suu
780	6	1.8	318	12	Q84147	Q84147 orf virus.
781	6	1.8	318	16	Q98G95	Q98g95 rhizobium l
782	6	1.8	319	10	Q9SXL5	Q9sx15 chlamydomon
783	6	1.8	319	10	Q9XHW4	Q9xhw4 oryza sativ
784	6	1.8	319	17	O26989	O26989 methanother
785	6	1.8	320	2	O30361	O30361 thermoanaer
786	6	1.8	320	5	O96620	O96620 drosophila
787	6	1.8	320	5	Q9NAH9	Q9nah9 caenorhabdi
788	6	1.8	320	16	Q9RTD7	Q9rtd7 deinococcus
789	6	1.8	320	17	O58066	O58066 pyrococcus
790	6	1.8	321	16	O31154	O31154 vibrio chol
791	6	1.8	321	16	Q9JXU5	Q9jxu5 neisseria m
792	6	1.8	321	16	Q9JW24	Q9jw24 neisseria m
793	6	1.8	321	16	Q9CF34	Q9cf34 lactococcus
794	6	1.8	321	17	Q9YCG0	Q9ycg0 aeropyrum p
795	6	1.8	322	5	Q961V5	Q961v5 drosophila
796	6	1.8	322	10	Q9S7P1	Q9s7p1 oryza sativ
797	6	1.8	322	16	Q9CP99	Q9cp99 pasteurella
798	6	1.8	323	5	Q9NKN7	Q9nkn7 leishmania
799	6	1.8	323	16	Q9CKC8	Q9ckc8 pasteurella
800	6	1.8	325	12	Q69501	Q69501 human herpe
801	6	1.8	325	13	Q90XK4	Q90xk4 pantodon bu
802	6	1.8	326	3	Q9HGY5	Q9hgy5 candida alb
803	6	1.8	326	10	Q9AU14	Q9au14 medicago tr
804	6	1.8	326	16	Q9CP26	Q9cp26 pasteurella
805	6	1.8	327	2	Q05083	Q05083 streptomyce
806	6	1.8	327	17	Q9V2H9	Q9v2h9 pyrococcus
807	6	1.8	328	4	Q96CA4	Q96ca4 homo sapien
808	6	1.8	328	4	Q96A43	Q96a43 homo sapien
809	6	1.8	328	16	Q9KRN4	Q9krn4 vibrio chol
810	6	1.8	328	16	Q9HY40	Q9hy40 pseudomonas
811	6	1.8	329	5	Q9TY08	Q9ty08 caenorhabdi
812	6	1.8	329	13	Q9IAY6	Q9iay6 sphoeroides
813	6	1.8	329	16	O35017	O35017 bacillus su
814	6	1.8	330	10	Q944B9	Q944b9 sambucus ni
815	6	1.8	330	11	P97269	P97269 cavia porce
816	6	1.8	330	16	Q92Y30	Q92y30 rhizobium m
817	6	1.8	330	16	Q92T17	Q92t17 rhizobium m
818	6	1.8	331	5	O17151	O17151 caenorhabdi
819	6	1.8	332	4	O60530	O60530 homo sapien

820	6	1.8	332	4	Q9H5L4	Q9h514 homo sapien
821	6	1.8	333	4	Q9BV77	Q9bv77 homo sapien
822	6	1.8	333	5	O45419	O45419 caenorhabdi
823	6	1.8	333	8	Q9T9H2	Q9t9h2 halocynthia
824	6	1.8	333	10	Q9ZT61	Q9zt61 sambucus ni
825	6	1.8	333	10	Q9ZT60	Q9zt60 sambucus ni
826	6	1.8	333	10	Q9SYS4	Q9sys4 sambucus ni
827	6	1.8	333	10	Q9SYS5	Q9sys5 sambucus ni
828	6	1.8	334	5	Q9VIS3	Q9vis3 drosophila
829	6	1.8	334	16	Q9KGG5	Q9kgg5 bacillus ha
830	6	1.8	334	17	O57833	O57833 pyrococcus
831	6	1.8	335	2	Q93RW6	Q93rw6 streptomyce
832	6	1.8	335	5	Q9N6L3	Q9n613 caenorhabdi
833	6	1.8	335	5	Q9NF70	Q9nf70 caenorhabdi
834	6	1.8	335	5	Q9NF69	Q9nf69 caenorhabdi
835	6	1.8	335	16	Q9HWY7	Q9hwy7 pseudomonas
836	6	1.8	335	16	Q99W79	Q99w79 staphylococ
837	6	1.8	336	2	O69606	O69606 moraxella s
838	6	1.8	336	5	Q21716	Q21716 caenorhabdi
839	6	1.8	336	10	Q944B8	Q944b8 sambucus ni
840	6	1.8	336	13	Q9YHW5	Q9yhw5 gallus gall
841	6	1.8	336	16	Q92VM9	Q92vm9 rhizobium m
842	6	1.8	337	4	Q9Y2S5	Q9y2s5 homo sapien
843	6	1.8	337	4	Q96C86	Q96c86 homo sapien
844	6	1.8	337	11	Q9CZW2	Q9czw2 mus musculu
845	6	1.8	337	11	P97268	P97268 cavia porce
846	6	1.8	337	16	Q9PEG4	Q9peg4 xylella fas
847	6	1.8	337	17	Q971J2	Q971j2 sulfolobus
848	6	1.8	338	11	Q9DAR7	Q9dar7 mus musculu
849	6	1.8	338	16	Q9AAU4	Q9aau4 caulobacter
850	6	1.8	338	16	Q98H37	Q98h37 rhizobium l
851	6	1.8	339	4	Q99772	Q99772 homo sapien
852	6	1.8	339	5	Q21788	Q21788 caenorhabdi
853	6	1.8	339	11	O70530	O70530 mus musculu
854	6	1.8	339	11	Q9D4F8	Q9d4f8 mus musculu
855	6	1.8	340	2	Q9KHK3	Q9khk3 streptomyce
856	6	1.8	340	2	Q9EWX3	Q9ewx3 streptomyce
857	6	1.8	341	16	Q9PFV1	Q9pfv1 xylella fas
858	6	1.8	341	16	Q99WW7	Q99ww7 staphylococ
859	6	1.8	341	16	Q92CU9	Q92cu9 listeria in
860	6	1.8	342	4	Q9BVR6	Q9bvr6 homo sapien
861	6	1.8	343	10	O22826	O22826 arabidopsis
862	6	1.8	343	16	Q986Q2	Q986q2 rhizobium l
863	6	1.8	344	8	Q94V75	Q94v75 lanthanotus
864	6	1.8	344	13	Q9PSJ1	Q9psj1 ictalurus p
865	6	1.8	344	13	Q98SH0	Q98sh0 ictalurus p
866	6	1.8	344	16	O34829	O34829 bacillus su
867	6	1.8	345	5	Q9Y161	Q9y161 drosophila
868	6	1.8	345	5	Q9XUR5	Q9xur5 caenorhabdi
869	6	1.8	345	10	Q9LS32	Q9ls32 physcomitre
870	6	1.8	345	11	Q9D790	Q9d790 mus musculu
871	6	1.8	346	2	O87156	O87156 vibrio chol
872	6	1.8	346	5	Q9W368	Q9w368 drosophila
873	6	1.8	346	16	Q9RVT6	Q9rvt6 deinococcus
874	6	1.8	346	16	Q9KA55	Q9ka55 bacillus ha
875	6	1.8	347	2	Q9S0N9	Q9s0n9 streptomyce
876	6	1.8	347	2	Q9ALP5	Q9alp5 bordetella
877	6	1.8	347	4	Q9NWL4	Q9nwl4 homo sapien
878	6	1.8	347	16	Q9CLB2	Q9clb2 pasteurella
879	6	1.8	348	4	Q96GZ7	Q96gz7 homo sapien
880	6	1.8	348	5	Q9UAH6	Q9uah6 caenorhabdi
881	6	1.8	348	5	Q9TXJ0	Q9txj0 caenorhabdi
882	6	1.8	348	12	Q9J5U2	Q9j5u2 o'nyong-nyo
883	6	1.8	348	12	Q9J5U1	Q9j5u1 o'nyong-nyo
884	6	1.8	349	2	Q56775	Q56775 xanthomonas
885	6	1.8	351	4	Q9C0F9	Q9c0f9 homo sapien
886	6	1.8	352	16	Q9I4W9	Q9i4w9 pseudomonas
887	6	1.8	353	5	Q9VLL7	Q9vll7 drosophila
888	6	1.8	353	13	Q9YHY3	Q9yhy3 lampetra fl
889	6	1.8	353	16	Q92ZP8	Q92zp8 rhizobium m
890	6	1.8	354	2	Q9XA39	Q9xa39 streptomyce
891	6	1.8	354	4	Q15867	Q15867 homo sapien
892	6	1.8	354	16	Q9I5Y7	Q9i5y7 pseudomonas
893	6	1.8	355	2	Q46402	Q46402 chlamydia t
894	6	1.8	355	3	Q05881	Q05881 saccharomyc
895	6	1.8	355	5	Q961C4	Q961c4 drosophila
896	6	1.8	355	7	Q30766	Q30766 macropus ru
897	6	1.8	355	16	Q9A7B8	Q9a7b8 caulobacter
898	6	1.8	356	2	O69155	O69155 streptococc
899	6	1.8	356	5	Q95SM5	Q95sm5 drosophila
900	6	1.8	356	16	Q99ZK3	Q99zk3 streptococc
901	6	1.8	356	16	Q97QP2	Q97qp2 streptococc
902	6	1.8	357	2	Q9L4N5	Q9l4n5 lactococcus
903	6	1.8	357	16	Q9CHR2	Q9chr2 lactococcus
904	6	1.8	357	16	Q9CF80	Q9cf80 lactococcus
905	6	1.8	358	10	Q9S7S1	Q9s7s1 arabidopsis
906	6	1.8	360	16	Q9A0C7	Q9a0c7 streptococc
907	6	1.8	361	10	Q9FIX4	Q9fix4 arabidopsis
908	6	1.8	361	16	Q98M55	Q98m55 rhizobium l
909	6	1.8	362	10	Q9FFW9	Q9ffw9 arabidopsis
910	6	1.8	363	5	Q9VB82	Q9vb82 drosophila
911	6	1.8	363	10	Q9M377	Q9m377 arabidopsis
912	6	1.8	363	17	O59026	O59026 pyrococcus
913	6	1.8	363	17	Q9V0D3	Q9v0d3 pyrococcus
914	6	1.8	364	2	Q9RDP0	Q9rdp0 streptomyce
915	6	1.8	364	16	Q98CR3	Q98cr3 rhizobium l
916	6	1.8	365	4	Q9H3E0	Q9h3e0 homo sapien
917	6	1.8	365	16	Q9RUH9	Q9ruh9 deinococcus
918	6	1.8	366	2	Q9Z504	Q9z504 streptomyce
919	6	1.8	366	5	Q95PB4	Q95pb4 ascaris suu
920	6	1.8	366	10	O04592	O04592 arabidopsis
921	6	1.8	366	17	Q97AP5	Q97ap5 thermoplasm
922	6	1.8	367	10	Q9FXT5	Q9fxt5 oryza sativ
923	6	1.8	367	10	Q9M166	Q9m166 arabidopsis
924	6	1.8	367	13	Q91905	Q91905 xenopus lae
925	6	1.8	369	8	O98998	O98998 vigna radia
926	6	1.8	370	3	Q96U81	Q96u81 neurospora
927	6	1.8	370	5	Q95U17	Q95u17 drosophila
928	6	1.8	370	13	Q91904	Q91904 xenopus lae
929	6	1.8	370	13	O57675	O57675 xenopus lae
930	6	1.8	371	5	O46052	O46052 drosophila
931	6	1.8	372	4	O60529	O60529 homo sapien
932	6	1.8	372	11	Q9CXT1	Q9cxt1 mus musculu
933	6	1.8	372	16	P95018	P95018 mycobacteri
934	6	1.8	373	4	Q96ML3	Q96ml3 homo sapien
935	6	1.8	373	8	Q9MU96	Q9mu96 ungeria flo
936	6	1.8	373	16	Q92WU5	Q92wu5 rhizobium m
937	6	1.8	374	10	Q9M2R9	Q9m2r9 arabidopsis
938	6	1.8	374	16	Q9PKY2	Q9pky2 chlamydia m
939	6	1.8	375	2	O66290	O66290 agrobacteri
940	6	1.8	375	17	Q978J3	Q978j3 thermoplasm
941	6	1.8	376	2	Q9Z6F5	Q9z6f5 vibrio para
942	6	1.8	376	2	Q9RGI6	Q9rgi6 bacteroides
943	6	1.8	376	6	Q95KI0	Q95ki0 macaca fasc
944	6	1.8	376	8	Q957A9	Q957a9 myotis levi
945	6	1.8	376	8	Q956Z7	Q956z7 myotis oxyo
946	6	1.8	376	16	Q9CCS1	Q9ccs1 mycobacteri
947	6	1.8	377	10	Q9FWU1	Q9fwu1 oryza sativ
948	6	1.8	377	16	Q9PE47	Q9pe47 xylella fas
949	6	1.8	378	16	O06423	O06423 mycobacteri
950	6	1.8	378	17	Q976U8	Q976u8 sulfolobus
951	6	1.8	379	5	Q20936	Q20936 caenorhabdi
952	6	1.8	379	8	Q957A8	Q957a8 myotis luci
953	6	1.8	379	8	Q956Z8	Q956z8 myotis nigr
954	6	1.8	379	8	Q956Z1	Q956z1 myotis vola
955	6	1.8	379	8	Q956Z0	Q956z0 myotis vola
956	6	1.8	380	8	Q33751	Q33751 arbacia lix
957	6	1.8	380	10	O81721	O81721 arabidopsis
958	6	1.8	380	16	Q9KT24	Q9kt24 vibrio chol
959	6	1.8	381	4	Q9Y408	Q9y408 homo sapien
960	6	1.8	381	5	Q20503	Q20503 caenorhabdi
961	6	1.8	381	10	Q9LDZ5	Q9ldz5 arabidopsis
962	6	1.8	382	5	Q9VV92	Q9vv92 drosophila
963	6	1.8	382	5	Q27438	Q27438 amblyomma a
964	6	1.8	383	8	Q94YZ6	Q94yz6 pylaiella l
965	6	1.8	383	16	O25795	O25795 helicobacte

966	6	1.8	383	16	Q9ZK33	Q9zk33 helicobacte
967	6	1.8	384	5	Q9N441	Q9n441 caenorhabdi
968	6	1.8	384	16	Q9A7D1	Q9a7d1 caulobacter
969	6	1.8	385	10	Q9C6K4	Q9c6k4 arabidopsis
970	6	1.8	385	16	Q99TE1	Q99te1 staphylococ
971	6	1.8	386	16	Q9A5M7	Q9a5m7 caulobacter
972	6	1.8	387	2	Q9ZII1	Q9zii1 streptococc
973	6	1.8	387	16	Q9KG75	Q9kg75 bacillus ha
974	6	1.8	388	2	Q54466	Q54466 streptomyce
975	6	1.8	388	4	Q96C95	Q96c95 homo sapien
976	6	1.8	388	16	Q9KNP8	Q9knp8 vibrio chol
977	6	1.8	389	2	P94200	P94200 azotobacter
978	6	1.8	389	11	Q91ZY3	Q91zy3 cavia porce
979	6	1.8	389	13	Q90WN1	Q90wn1 xenopus lae
980	6	1.8	389	16	Q9HWY6	Q9hwy6 pseudomonas
981	6	1.8	390	2	P95540	P95540 pediococcus
982	6	1.8	390	2	O50279	O50279 pseudomonas
983	6	1.8	390	2	Q93DB5	Q93db5 agrobacteri
984	6	1.8	390	6	Q9GMX0	Q9gmx0 macaca fasc
985	6	1.8	390	10	Q9LYG5	Q9lyg5 arabidopsis
986	6	1.8	390	16	Q9I324	Q9i324 pseudomonas
987	6	1.8	391	2	Q9X684	Q9x684 pseudomonas
988	6	1.8	391	2	Q9X685	Q9x685 pseudomonas
989	6	1.8	391	2	O86769	O86769 streptomyce
990	6	1.8	391	2	P95475	P95475 pseudomonas
991	6	1.8	391	5	Q9VUJ5	Q9vuj5 drosophila
992	6	1.8	391	11	Q9ESS9	Q9ess9 rattus norv
993	6	1.8	391	11	Q91WR9	Q91wr9 mus musculu
994	6	1.8	391	16	Q98IM6	Q98im6 rhizobium l
995	6	1.8	392	2	O30529	O30529 pseudomonas
996	6	1.8	392	2	Q9RJL7	Q9rjl7 streptomyce
997	6	1.8	392	16	Q9CEQ8	Q9ceq8 lactococcus
998	6	1.8	393	2	Q9LAZ3	Q9laz3 streptococc
999	6	1.8	393	2	Q9RNH2	Q9rnh2 rhodobacter
1000	6	1.8	393	16	Q92WC3	Q92wc3 rhizobium m

ALIGNMENTS

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RESULT   1
Q20468
ID   Q20468      PRELIMINARY;      PRT;   137 AA.
AC   Q20468;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   F46F2.3 PROTEIN.
GN   F46F2.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Thomas K.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z69903; CAA93772.1; -.
SQ   SEQUENCE   137 AA;  14265 MW;  46CBDD4ABE352114 CRC64;


  Query Match             2.7%;  Score 9;  DB 5;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 0.56;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    126 QQPAYQPQP 134
          |||||||||
Db     67 QQPAYQPQP 75


RESULT   2
Q9WLL1
ID   Q9WLL1      PRELIMINARY;      PRT;   522 AA.
AC   Q9WLL1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GAG PROTEIN.
GN   GAG.
OS   Mus dunni endogenous virus.
OC   Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX   NCBI_TaxID=75986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98362151; PubMed=9696842;
RA   Wolgamot G., Bonham L., Miller A.D.;
RT   "Sequence analysis of Mus dunni endogenous virus reveals a hybrid
RT   VL30/Gibbon ape leukemia virus-like structure and a distinct
RT   envelope.";
RL   J. Virol. 72:7459-7466(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Wolgamot G., Bonham L., Miller A.D.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF053745; AAC31804.1; -.
DR   InterPro; IPR000840; Gag_MA.
DR   InterPro; IPR003036; Gag_p30.
DR   InterPro; IPR001878; Znf_CCHC.
DR   Pfam; PF01140; gag_MA; 1.
DR   Pfam; PF02093; Gag_p30; 1.
DR   Pfam; PF00098; zf-CCHC; 1.
DR   SMART; SM00343; ZnF_C2HC; 1.
KW   Core protein; Polyprotein; Zinc-finger.
SQ   SEQUENCE   522 AA;  58597 MW;  0E7A04D31969B81C CRC64;


  Query Match             2.7%;  Score 9;  DB 15;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    169 PVAAPQPEP 177
          |||||||||
Db    156 PVAAPQPEP 164


RESULT   3
O89814
ID   O89814      PRELIMINARY;      PRT;   622 AA.
AC   O89814;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GLYCOSYLATED GAG PROTEIN.
GN   GAG.
OS   Mus dunni endogenous virus.
OC   Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX   NCBI_TaxID=75986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98362151; PubMed=9696842;
RA   Wolgamot G., Bonham L., Miller A.D.;
RT   "Sequence analysis of Mus dunni endogenous virus reveals a hybrid
RT   VL30/Gibbon ape leukemia virus-like structure and a distinct
RT   envelope.";
RL   J. Virol. 72:7459-7466(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Wolgamot G., Bonham L., Miller A.D.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; AF053745; AAC31803.1; -.
DR   InterPro; IPR000840; Gag_MA.
DR   InterPro; IPR003036; Gag_p30.
DR   InterPro; IPR001878; Znf_CCHC.
DR   Pfam; PF01140; gag_MA; 1.
DR   Pfam; PF02093; Gag_p30; 1.
DR   Pfam; PF00098; zf-CCHC; 1.
DR   SMART; SM00343; ZnF_C2HC; 1.
KW   Core protein; Polyprotein; Zinc-finger.
SQ   SEQUENCE   622 AA;  69125 MW;  159BCFB052106CD3 CRC64;


  Query Match             2.7%;  Score 9;  DB 15;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    169 PVAAPQPEP 177
          |||||||||
Db    256 PVAAPQPEP 264


RESULT   4
Q9HNM8
ID   Q9HNM8      PRELIMINARY;      PRT;   130 AA.
AC   Q9HNM8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VNG2029H.
GN   VNG2029H.
OS   Halobacterium sp. (strain NRC-1).
OC   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC   Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR   EMBL; AE005096; AAG20192.1; -.
KW   Complete proteome.
SQ   SEQUENCE   130 AA;  12950 MW;  91FF13451FD59892 CRC64;


  Query Match             2.4%;  Score 8;  DB 17;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    166 PAEPVAAP 173
          ||||||||
Db     74 PAEPVAAP 81


RESULT   5
Q9XYB2
ID   Q9XYB2      PRELIMINARY;      PRT;   210 AA.
AC   Q9XYB2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MEROZOITE SURFACE PROTEIN 4/5.
GN   MSP4/5.
OS   Plasmodium chabaudi adami.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5826;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DS;
RX   MEDLINE=99242782; PubMed=10225857;
RA   Black C.G., Wang L., Hibbs A.R., Werner E., Coppel R.L.;
RT   "Identification of the Plasmodium chabaudi homologue of merozoite
RT   surface proteins 4 and 5 of Plasmodium falciparum.";
RL   Infect. Immun. 67:2075-2081(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DS;
RX   MEDLINE=20078867; PubMed=10613706;
RA   Kedzierski L., Black C.G., Coppel R.L.;
RT   "Characterization of the merozoite surface protein 4/5 gene of
RT   Plasmodium berghei and Plasmodium yoelii.";
RL   Mol. Biochem. Parasitol. 105:137-147(2000).
DR   EMBL; AF080446; AAD28328.1; -.
DR   InterPro; IPR000561; EGF-like.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ   SEQUENCE   210 AA;  22279 MW;  49364EF8EA2ACD42 CRC64;


  Query Match             2.4%;  Score 8;  DB 5;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     14 AIAIIALL 21
          ||||||||
Db    202 AIAIIALL 209


RESULT   6
Q9ADC6
ID   Q9ADC6      PRELIMINARY;      PRT;   222 AA.
AC   Q9ADC6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SPDA2 PROTEIN.
GN   SPDA2.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Saunders D.C., Harris D.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL589707; CAC33905.1; -.
SQ   SEQUENCE   222 AA;  23251 MW;  B74F3719B4BF310A CRC64;


  Query Match             2.4%;  Score 8;  DB 2;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 9.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    177 PVAEPAPV 184
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          ||||||||
Db    159 PVAEPAPV 166


RESULT   7
Q92LX9
ID   Q92LX9      PRELIMINARY;      PRT;   234 AA.
AC   Q92LX9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC03152.
GN   SMC03152.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21368234; PubMed=11474104;
RA   Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA   Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA   Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA   Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA   Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA   Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA   Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA   Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA   Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA   Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT   "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL   Science 293:668-672(2001).
DR   EMBL; AL591792; CAC47462.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   234 AA;  23951 MW;  441A880844492F44 CRC64;


  Query Match             2.4%;  Score 8;  DB 16;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 9.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    176 EPVAEPAP 183
          ||||||||
Db     86 EPVAEPAP 93


RESULT   8
Q95RV8
ID   Q95RV8      PRELIMINARY;      PRT;   400 AA.
AC   Q95RV8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LD09043P.
GN   ACF1.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY061103; AAL28651.1; -.
SQ   SEQUENCE   400 AA;  46108 MW;  84BFE4E8F8FFDC5D CRC64;


  Query Match             2.4%;  Score 8;  DB 5;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     54 DEDVEDDE 61
          ||||||||
Db     93 DEDVEDDE 100


RESULT   9
Q9S333
ID   Q9S333      PRELIMINARY;      PRT;   431 AA.
AC   Q9S333;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 46.3 KDA PROTEIN.
GN   ORF431.
OS   Prochlorococcus marinus.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1219;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CCMP 1375;
RX   MEDLINE=97008144; PubMed=8855320;
RA   Hess W.R., Partensky F., van der Staay G.W., Garcia-Fernandez J.M.,
RA   Boerner T., Vaulot D.;
RT   "Coexistence of phycoerythrin and a chlorophyll a/b antenna in a
RT   marine prokaryote.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11126-11130(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CCMP 1375;
RX   MEDLINE=99364545; PubMed=10437834;
RA   Hess W.R., Steglich C., Lichtle C., Partensky F.;
RT   "Phycoerythrins of the oxyphotobacterium Prochlorococcus marinus are
RT   associated to the thylakoid membrane and are encoded by a single large
RT   gene cluster.";
RL   Plant Mol. Biol. 40:507-521(1999).
DR   EMBL; AJ001230; CAB52700.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   431 AA;  46291 MW;  B2D73641FA95F729 CRC64;


  Query Match             2.4%;  Score 8;  DB 2;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     10 IIVGAIAI 17
          ||||||||
Db    138 IIVGAIAI 145


RESULT  10
O57311
ID   O57311      PRELIMINARY;      PRT;   441 AA.
AC   O57311;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ZINC FINGER PROTEIN ZIC 3 (ZINC FINGER PROTEIN OF THE CEREBELLUM 3)
DE   (ZIC3 PROTEIN).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98004509; PubMed=9342348;
RA   Nakata K., Nagai T., Aruga J., Mikoshiba K.;
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RT   "Xenopus Zic3, a primary regulator both in neural and neural crest
RT   development.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:11980-11985(1997).
RN   [2]
RP   REVISIONS.
RA   Nakata K., Nagai T., Aruga J., Mikoshiba K.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CAN DETERMINE THE ECTODERMAL CELL FATE AND PROMOTE THE
CC       EARLIEST STEP OF NEURAL AND NEURAL CREST DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- TISSUE SPECIFICITY: CNS. A HIGH LEVEL EXPRESSION IS SEEN IN THE
CC       CEREBELLUM.
CC   -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT EARLY GASTRULA IN DORSAL
CC       LIP AND PROSPECTIVE NEURAL PLATE. IT THEN DECREASED IN THE DORSAL
CC       LIP AND INCREASED IN THE PROSPECTIVE NEURAL PLATE. AT THE NEURAL
CC       PLATE STAGE, IT IS EXPRESSED STRONGLY IN PROSPECTIVE REGION OF
CC       MESENCEPHALON AND ANTERIOR RHOMBENCEPHALON. AT EARLY TAILBUD
CC       STAGES, IT BECAME RESTRICTED TO THE DORSAL REGION OF FOREBRAIN,
CC       MIDBRAIN, AND HINDBRAIN, AND WEAKLY TO THE DORSAL REGION OF THE
CC       TRUNK. AFTER MID-TAILBUD STAGE, IT DECREASED IN THE DIENCEPHALON,
CC       APPEARED IN THE LATERAL MESODERM OF THE TAILBUD REGION AND IS
CC       RESTRICTED IN THE DORSAL PART OF THE NEURAL TUBE.
CC   -!- SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS
CC       PROTEINS.
DR   EMBL; AB005292; BAA23874.2; -.
DR   HSSP; P08047; 1SP2.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 5.
DR   SMART; SM00355; ZnF_C2H2; 5.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   Developmental protein; Neurogenesis; Zinc-finger; Metal-binding;
KW   DNA-binding; Repeat; Nuclear protein; Multigene family.
FT   ZN_FING     222    257       C2H2-TYPE (ATYPICAL).
FT   ZN_FING     266    293       C2H2-TYPE (ATYPICAL).
FT   ZN_FING     299    323       C2H2-TYPE.
FT   ZN_FING     329    353       C2H2-TYPE.
FT   ZN_FING     359    381       C2H2-TYPE.
SQ   SEQUENCE   441 AA;  48481 MW;  FB8F340A2E3EDA4E CRC64;


  Query Match             2.4%;  Score 8;  DB 13;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     197 MNVAAHHG 204
           ||||||||
Db     199 MNVAAHHG 206


RESULT  11
Q9SSF3
ID   Q9SSF3      PRELIMINARY;      PRT;   457 AA.
AC   Q9SSF3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MLP3.2 PROTEIN.
GN   MLP3.2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA   Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT   "Arabidopsis thaliana chromosome III P1 MLP3 genomic sequence.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC009176; AAF13075.1; -.
SQ   SEQUENCE   457 AA;  50356 MW;  03564C83112632CA CRC64;


  Query Match             2.4%;  Score 8;  DB 10;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 ILIIVGAI 15
             ||||||||
Db     223 ILIIVGAI 230


RESULT  12
Q9CGA7
ID   Q9CGA7      PRELIMINARY;      PRT;   512 AA.
AC   Q9CGA7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   CITRATE LYASE ALPHA CHAIN (EC 4.1.3.6).
GN   CITF.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006351; AAK05289.1; -.
KW   Lyase; Complete proteome.
SQ   SEQUENCE   512 AA;  55440 MW;  AF6851813614CDC4 CRC64;


  Query Match             2.4%;  Score 8;  DB 16;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     318 DIIREVKD 325
           ||||||||
Db     505 DIIREVKD 512


RESULT  13
Q9VKL0
ID   Q9VKL0      PRELIMINARY;      PRT;   620 AA.
AC   Q9VKL0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CG14917 PROTEIN.
GN   SAMUEL OR CG12291 OR CG14917 OR CG14918.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003630; AAF53057.1; -.
DR FlyBase; FBgn0032330; Samuel.
SQ SEQUENCE 620 AA; 62463 MW; DFD8BA827FFD385D CRC64;

Query Match 2.4%; Score 8; DB 5; Length 620;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 212 LLNSIQQA 219
||||||||
Db 101 LLNSIQQA 108

RESULT 14
Q9Y0W1
ID Q9Y0W1 PRELIMINARY; PRT; 1476 AA.
AC Q9Y0W1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE ATP-DEPENDENT CHROMATIN ASSEMBLY FACTOR LARGE SUBUNIT.
GN ACF1 OR CG1966.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315627; PubMed=10385622;
RA Ito T., Levenstein M.E., Fyodorov D.V., Kutach A.K., Kobayashi R.,
RA Kadonaga J.T.;
RT "ACF consists of two subunits, Acf1 and ISWI, that function
RT cooperatively in the ATP-dependent catalysis of chromatin assembly.";
RL Genes Dev. 13:1529-1539(1999).
DR EMBL; AF148962; AAD38952.1; -.
DR FlyBase; FBgn0027620; Acf1.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR004022; DDT.
DR InterPro; IPR001965; PHD.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF00628; PHD; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00249; PHD; 2.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ SEQUENCE 1476 AA; 170457 MW; C18A6CEBF57E66B3 CRC64;

Query Match 2.4%; Score 8; DB 5; Length 1476;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 DEDVEDDE 61
||||||||
Db 1169 DEDVEDDE 1176

RESULT 15
Q9V9T4
ID Q9V9T4 PRELIMINARY; PRT; 1476 AA.
AC Q9V9T4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE ACF1 PROTEIN.
GN ACF1 OR CG1966.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

```
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003779; AAF57200.1; -.
DR   FlyBase; FBgn0027620; Acf1.
DR   InterPro; IPR001487; Bromodomain.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR004022; DDT.
DR   InterPro; IPR001965; PHD.
DR   Pfam; PF00439; bromodomain; 1.
DR   Pfam; PF00628; PHD; 2.
DR   PRINTS; PR00503; BROMODOMAIN.
DR   SMART; SM00297; BROMO; 1.
DR   SMART; SM00249; PHD; 2.
DR   PROSITE; PS50014; BROMODOMAIN_2; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ   SEQUENCE   1476 AA;  170410 MW;  9EE1906672E5B006 CRC64;


  Query Match             2.4%;  Score 8;  DB 5;  Length 1476;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      54 DEDVEDDE 61
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Db    1169 DEDVEDDE 1176


Search completed: September 25, 2002, 09:56:57
Job time: 256 sec
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